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(54) Title: CRYSTAL STRUCTURE OF BACE AND USES THEREOF

(57) Abstract: This invention is directed to the three dimensional crystal structure of Beta-site APP Cleaving Enzyme (BACE), and to the use of this structure in rational drug design methods to identify agents that may interact with active sites of BACE. Such agents may represent new therapeutics in the treatment and/or prevention of Alzheimer's Disease.

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CRYSTAL STRUCTURE OF BACE AND USES THEREOF

Field of the Invention

[0001] The present invention relates to the three dimensional crystal structure of Beta-site APP Cleaving Enzyme (BACE), and to the use of this structure in rational drug design methods to identify agents that may interact with active sites of BACE. Such agents may represent new therapeutics in the treatment and/or prevention of Alzheimer's Disease.

Background of the Invention

[0002] A characteristic pathology of Alzheimer's Disease is the build up of insoluble amyloid plaques in the brain. These proteinaceous plaques are composed of a 4KDa, 42 amino acid fragment of β-Amyloid Precursor Protein (APP) and is termed Amyloid β-peptide (Aβ). The mechanism of Aβ production is hence of critical importance in understanding the onset and progress of Alzheimer's Disease. It has been shown that Aβ is derived from the proteolytic cleavage of a larger protein, β-amyloid precursor protein (APP). Two enzymes are responsible for this cleavage; first, the enzyme β-secretase cleaves APP at residue 671 (770aa isoform of APP numbering) and then γ-secretase cleaves at residue 716. More recently, the novel transmembrane aspartic protease BACE has been identified as being β-secretase. This protein is now a significant target in a therapeutic approach to Alzheimer's Disease. In rare cases of Alzheimer's Disease that are hereditary (Familial Alzheimer's Disease (FAD)) the disease phenotype has been isolated to mutations in the β-Amyloid Precursor Protein. One particular cohort, the 'Swedish mutation', exhibits a double mutation at the β-secretase cleavage site.

[0003] Based upon the role of BACE in Alzheimer's Disease, the elucidation of the three-dimensional structure of BACE, as well as its site of binding with APP, would have important implications in the treatment and/or prevention of Alzheimer's Disease and similar diseases associated with the

presence of insoluble amyloid plaques composed the 42 amino acid fragment of APP in the brain.

Summary of the Invention

[0004] The present invention provides a crystal of BACE complexed with an APP inhibitor peptide, as well as the three dimensional structure of BACE as derived by x-ray diffraction data of the BACE/APP inhibitor peptide crystal. Specifically, the three dimensional structure of BACE is defined by the structural coordinates shown in Figure 1, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å. The structural coordinates of BACE are useful for a number of applications, including, but not limited to, the visualization, identification and characterization of various active sites of BACE, and the BACE/APP inhibitor peptide complex, including the APP binding site. The active site structures may then be used to design various agents which interact with BACE, as well as BACE complexed with an APP protein or peptide, or related molecules.

[0005] The present invention is also directed to an active site of an APP binding protein or peptide, and preferably the APP peptide binding site of BACE that is elucidated and derived from the three dimensional structure of BACE as defined by the relative structural coordinates set forth in Figure 1, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

[0006] In one embodiment of the present invention, the active site of the APP binding protein or peptide, preferably the APP peptide binding site of BACE, comprises the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

[0007] In another embodiment, the active site of the APP binding protein or peptide, preferably the APP peptide binding site of BACE, comprises the

relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

[0008] The present invention further provides a method for identifying an agent that interacts with an active site of BACE. The method comprises the steps of: (a) determining a putative active site of BACE from a three dimensional model of BACE using the relative structural coordinates of Figure 1, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å; and (b) performing various computer fitting analyses to identify an agent which interacts with the putative active site.

[0009] The present invention also provides method for identifying an agent that interacts with an active site of an APP binding protein or peptide, preferably BACE. The method comprises the steps of: (a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and (b) designing an agent using the three dimensional model generated in step (a).

[0010] The present invention also provides another method for identifying an agent that interacts with an active site of an APP binding protein or peptide, preferably BACE. The method comprises the steps of: (a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and (b) designing an agent using the three dimensional model generated in step (a).

[0011] Finally, the present invention provides agents, and preferably inhibitors, identified using the foregoing methods. Small molecules or other agents which inhibit or otherwise interfere with the ability of BACE to cleave APP may be useful in the treatment and/or prevention of Alzheimer's Disease.

[0012] Additional objects of the present invention will be apparent from the description which follows.

Brief Description of the Figure

[0013] Figure 1 provides the atomic structural coordinates for BACE and the APP inhibitor peptide as derived by X-ray diffraction of a crystal of the BACE and APP inhibitor peptide complex. "Atom type" refers to the atom whose coordinates are being measured. "Residue" refers to the type of residue of which each measured atom is a part - i.e., amino acid, cofactor, ligand or solvent. The

"x, y and z" coordinates indicate the Cartesian coordinates of each measured atom's location in the unit cell (Å). "Occ" indicates the occupancy factor. "B" indicates the "B-value", which is a measure of how mobile the atom is in the atomic structure ($Å^2$).

Detailed Description of the Invention

[0014] As used herein, the following terms and phrases shall have the meanings set forth below:

[0015] Unless otherwise noted, "BACE" is Beta-site APP Cleaving Enzyme, and is the β-secretase enzyme that cleaves β-amyloid precursor protein (APP) at residue 671 (770aa isoform of APP numbering). After cleavage of APP by BACE, the remaining APP is cleaved at residue 716 by γ-secretase, leaving a 42 amino acid fragment of APP that is found in the proteinaceous plaques of Alzheimer's patients. The amino acid sequence of BACE preferably has the amino acid sequence deposited with Swiss Prot under accession number P56817, including conservative substitutions. As used herein, BACE also includes "BACE peptides," which are molecules having less than the complete amino acid sequence of BACE. Preferably, BACE peptides include the active site in which BACE binds to and cleaves APP. Most preferably, the BACE peptide corresponds to amino acid residues 58-447 set forth in Figure 1 ("$BACE_{58-447}$"), including conservative substitutions.

[0016] "APP" is β-amyloid precursor protein having the amino acid sequence deposited with Swiss Prot under accession number CAA31830, including conservative substitutions. As used herein, APP also includes "APP peptides," which are molecules having less than the complete amino acid sequence of APP. Preferably, APP peptides include the active site in which APP is cleaved by BACE.

[0017] An "APP inhibitor peptide" is a peptide which inhibits binding between BACE and APP. Preferably, the APP peptide has the amino acid sequence SER-GLU-VAL-ASN-Sta-VAL-ALA-GLU-PHE, where Sta is rare amino acid (S)-Statine.

[0018] An "APP binding protein or peptide" is a protein or peptide that binds APP and has a APP binding site, and includes but is not limited to BACE and BACE peptides.

[0019] Unless otherwise indicated, "protein" shall include a protein, protein domain, polypeptide or peptide.

[0020] "Structural coordinates" are the Cartesian coordinates corresponding to an atom's spatial relationship to other atoms in a molecule or molecular complex. Structural coordinates may be obtained using x-ray crystallography techniques or NMR techniques, or may be derived using molecular replacement analysis or homology modeling. Various software programs allow for the graphical representation of a set of structural coordinates to obtain a three dimensional representation of a molecule or molecular complex. The structural coordinates of the present invention may be modified from the original set provided in Figure 1 by mathematical manipulation, such as by inversion or integer additions or subtractions. As such, it is recognized that the structural coordinates of the present invention are relative, and are in no way specifically limited by the actual x, y, z coordinates of Figure 1.

[0021] An "agent" shall include a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound or drug.

[0022] "Root mean square deviation" is the square root of the arithmetic mean of the squares of the deviations from the mean, and is a way of expressing deviation or variation from the structural coordinates of BACE described herein. The present invention includes all embodiments comprising conservative substitutions of the noted amino acid residues resulting in same structural coordinates within the stated root mean square deviation.

[0023] The numbering of the amino acid residues identified in Figure 1 are based on the numbering of the full length BACE protein from the start of the signal sequence. It will be obvious to the skilled practitioner that the numbering of the amino acid residues of BACE may be different than that set forth herein or may contain certain conservative amino acid substitutions that yield the same

three dimensional structures as those defined in Figure 1. Corresponding amino acids and conservative substitutions in other isoforms or analogues are easily identified by visual inspection of the relevant amino acid sequences or by using commercially available homology software programs (e.g., MODELLAR, MSI, San Diego, CA).

[0024] "Conservative substitutions" are those amino acid substitutions which are functionally equivalent to the substituted amino acid residue, either by way of having similar polarity, steric arrangement, or by belonging to the same class as the substituted residue (e.g., hydrophobic, acidic or basic) and includes substitutions having an inconsequential effect on the three dimensional structure of BACE, with respect to the use of this structure for the identification and design of agents which interact with BACE, for molecular replacement analyses and/or for homology modeling.

[0025] As used herein, an "active site" refers to a region of a molecule or molecular complex that, as a result of its shape and charge potential, favorably interacts or associates with another agent (including, without limitation, a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, antibiotic or drug) via various covalent and/or non-covalent binding forces. Preferably, the active site of BACE corresponds to the site in which BACE cleaves the APP molecule.

[0026] As such, the active site of BACE may include, for example, both the actual site in which BACE binds and cleaves APP, as well as accessory binding sites adjacent or proximal to the actual binding site that nonetheless may affect the ability of BACE to bind and cleave APP, either by direct interference with the actual site of binding or by indirectly affecting the steric conformation or charge potential of the BACE molecule and thereby preventing or reducing the ability of BACE to bind to APP at the actual binding site. As used herein, an active site also includes BACE or BACE analog residues which exhibit observable NMR perturbations in the presence of a binding ligand, such as APP or an APP peptide. While such residues exhibiting observable NMR perturbations may not necessarily be in direct contact with or immediately

proximate to ligand binding residues, they may be critical to BACE residues for rational drug design protocols.

[0027] The present invention is directed to a crystallized complex of BACE and an APP inhibitor peptide that effectively diffracts X-rays for the determination of the structural coordinates of the complex. As used herein, BACE preferably corresponds to $BACE_{58-447}$ as set forth in Figure 1, with the N-terminal domain consisting of amino acid residues 58-207 shown in Figure 1, and the C-terminal domain consisting of amino acid residues 208-447 shown in Figure 1. The APP inhibitor peptide is preferably SER-GLU-VAL-ASN-Sta-VAL-ALA-GLU-PHE.

[0028] Using the crystal complex of the present invention, X-ray diffraction data can be collected by a variety of means in order to obtain the atomic coordinates of the crystallized molecule or molecular complex. With the aid of specifically designed computer software, such crystallographic data can be used to generate a three dimensional structure of the molecule or molecular complex. Various methods used to generate and refine the three dimensional structure of a crystallized molecule or molecular structure are well known to those skilled in the art, and include, without limitation, multiwavelength anomalous dispersion (MAD), multiple isomorphous replacement, reciprocal space solvent flattening, molecular replacement, and single isomorphous replacement with anomalous scattering (SIRAS).

[0029] Accordingly, the present invention also provides the three dimensional structure of BACE as derived by x-ray diffraction data of the BACE/APP inhibitor peptide crystal. Specifically, the three dimensional structure of BACE is defined by the structural coordinates shown in Figure 1, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, preferably not more than 1.0Å, and most preferably not more than 0.5Å. The structural coordinates of BACE are useful for a number of applications, including, but not limited to, the visualization, identification and characterization of various active sites of BACE, and the BACE/APP inhibitor peptide complex, including the APP or APP peptide binding site. The active site

structures may then be used to design agents with interact with BACE, as well as BACE complexed with APP, an APP peptide or related molecules.

[0030] The present invention is also directed to an active site of an APP binding protein or peptide, preferably the APP peptide binding site of BACE, which comprises the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å.

[0031] In another preferred embodiment, the active site of an APP binding protein or peptide, preferably the APP peptide binding site of BACE, comprises the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å.

[0032] Another aspect of the present invention is directed to a method for identifying an agent that interacts with an active site of BACE comprising the steps of: (a) determining an active site of BACE from a three dimensional model of BACE using the relative structural coordinates of Figure 1, ± a root mean square deviation from the backbone atoms of said amino acids of not more than

1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å; and (b) performing computer fitting analysis to identify an agent which interacts with said active site. Computer fitting analyses utilize various computer software programs that evaluate the "fit" between the putative active site and the identified agent, by (a) generating a three dimensional model of the putative active site of a molecule or molecular complex using homology modeling or the atomic structural coordinates of the active site, and (b) determining the degree of association between the putative active site and the identified agent. Three dimensional models of the putative active site may be generated using any one of a number of methods known in the art, and include, but are not limited to, homology modeling as well as computer analysis of raw data generated using crystallographic or spectroscopy data. Computer programs used to generate such three dimensional models and/or perform the necessary fitting analyses include, but are not limited to: GRID (Oxford University, Oxford, UK), MCSS (Molecular Simulations, San Diego, CA), AUTODOCK (Scripps Research Institute, La Jolla, CA), DOCK (University of California, San Francisco, CA), Flo99 (Thistlesoft, Morris Township, NJ), Ludi (Molecular Simulations, San Diego, CA), QUANTA (Molecular Simulations, San Diego, CA), Insight (Molecular Simulations, San Diego, CA), SYBYL (TRIPOS, Inc., St. Louis. MO) and LEAPFROG (TRIPOS, Inc., St. Louis, MO).

[0033] The present invention also provides a method for identifying an agent that interacts with an active site of an APP binding protein or peptide, and preferably the APP peptide binding site on BACE. The method comprises the steps of: (a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å;

and (b) designing an agent using the three dimensional model generated in step (a). In another preferred embodiment, the active site of the APP binding protein or peptide is generated using the three dimensional model defined by the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å.

[0034] The effect of such an agent identified by computer fitting analyses on the APP binding protein or peptide may be further evaluated by obtaining or synthesizing the agent, and contacting the identified agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide. Preferably, the APP binding protein or peptide is BACE (or a BACE peptide), and the agent is a potential inhibitor of binding between BACE (or a BACE peptide) and APP (or an APP peptide). Therefore, in the preferred embodiment, the agent is contacted with BACE (or a BACE peptide) in the presence of APP (or a APP peptide), to determine the ability of the agent to inhibit binding between BACE (or the BACE peptide) and APP (or the APP peptide). Depending upon the action of the agent on the active site, the agent may act either as an inhibitor or activator of the BACE/APP binding. Assays may be performed and the results analyzed to determine whether the agent is an inhibitor (i.e., the agent may reduce or prevent binding affinity between BACE and APP), an activator (i.e., the agent may increase binding

affinity between BACE and APP), or has no effect on the interaction between BACE and APP. Agents identified using the foregoing methods, and preferably inhibitors of BACE cleavage of APP, may then be tested as therapeutics in the treatment and/or prevention of Alzheimer's Disease, and other diseases that are also characterized by the presence of the 42 amino acid fragment of APP in the proteinaceous plaques of the brain.

[0035] Various molecular analysis and rational drug design techniques are further disclosed in U.S. Patent Nos. 5,834,228, 5,939,528 and 5,865,116, as well as in PCT Application No. PCT/US98/16879, published WO 99/09148, the contents of which are hereby incorporated by reference.

[0036] Finally, the present invention is also directed to the agents, and preferably the inhibitors, identified using the foregoing methods. Such agents may be a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, or drug, and preferably are small molecules that effectively inhibit binding between BACE and APP or an APP peptide. Such molecules may be useful in treating, preventing or inhibiting progression of Alzheimer's Disease.

[0037] The present invention may be better understood by reference to the following non-limiting Example. The following Example is presented in order to more fully illustrate the preferred embodiments of the invention, and should in no way be construed as limiting the scope of the present invention.

Example 1

A. Methods

[0038] Cloning of Human BACE1. Human polyA+ mRNA from whole brain (Clontech) was converted to cDNA by random-priming using Thermoscript RT-PCR System, according to the manufacturer's protocol (Lifetechnologies). This cDNA was amplified by PCR using the forward and reverse primers, 5' GCTCTAGAACCCAGC ACGGCATCCGGCTG 3' (XbaI site indicated by underlined sequence; nts. 517-537 in accession no. AF190725) and 5' CCAAGCATGCGGCCGCAATAGGCTATGGTCA TGAGGGTTGAC 3' (NotI site

indicated by underlined sequence; nts. 1809-1833; bold "A" indicates additional nucleotide to permit in-frame translation of the Fc chimera; see below), respectively. PCR was accomplished using Expand Long Polymerase kit according to the manufacturer's conditions (Roche Biochemicals; buffer #3), with PCR cycling consisting of an initial denaturing step at 95°C for 3min, 30-40 cycles of denaturation at 94°C for 30sec, annealing at 65°C for 30sec, elongation at 68°C for 1min 30sec, followed by a final elongation at 68°C for 5min. The PCR products were run on a 1% agarose gel. The appropriate band was cut out of the gel, purified by Quantum Prep Freeze 'N Squeeze DNA Extraction Columns (Bio-Rad), and cloned into the SpeI/NotI sites of the mammalian expression vector, pED/Fc (Kaufman, RJ et al., 1991, Nucl. Acids. Res. 19:4485-4490).

[0039] An intermediate construct contained the honey bee meletin secretory leader fused to the the prodomain and coding region of BACE1, just upstream to the predicted transmembrane domain of BACE1 (Vassar, R. et al., 1999, Science 286:735-741). The absence of the predicted hydrophobic transmembrane domain in this construct would permit soluble secreted BACE.Fc protein to be extracted from the conditioned medium. Downstream of BACE1 was an engineered enterokinase cleavage site followed by sequence encoding the Fc portion of immunoglobulin IgG. The final construct contained the BACE1.Fc gene, flanked by SalI and EcoRI in pED/Fc, cloned into the SalI/EcoRI sites of the mammalian expression vector, pHTop, a derivative of pED, in which the majority of the adenovirus major late promoter was replaced by six repeats of a bacterial tetracycline operator (described in Gossen et al, 1992, PNAS, 89:5547-5551). Sequencing of the BACE1.Fc recombinant gene was accomplished by BigDye terminator dideoxy sequencing using an ABI3700. Sequence analyses was accomplished using DNAstar software package.

[0040] Expression of Human BACE1. The vector, pHTOP, with the BACE1.Fc insert, contains the dihydrofolate reductase gene and when introduced in the cell line CHO/A2 (see description below) functions very

efficiently and high expressers can be selected by isolating cells surviving in high methotrexate concentrations.The CHO/A2 cell line is derived from CHO DUKX B11 (Urlaub and Chasin, 1980, PNAS USA 77:4216-4220) by stably integrating a transcriptional activator (tTA), a fusion protein between the Tet repressor and the herpes virus VP16 transcriptional domain (Gossen et al). A CHO cell line expressing extracellular BACE1.Fc was established by transfecting (lipofection) pHTopBACE1.Fc into CHO/A2 cells and selecting clones in 0.02 and 0.05 μM methotrexate. The conditioned media from multiple clones were screened by Western blot using a (mouse) anti-human IgG.Fc HRP antibody. The same clones were also metabolically labeled with 35 S (met/cys). The best clone, determined by virtue of its high expression, was one which resulted from 0.05 μM MTX selection and was chosen to be scaled up for roller bottle conditioned media production (4 Liters). The conditioned media was then used for purification. The expressed protein has residues 22-460 and nine extra residues at the C-terminal (an artefact from cloning and remains of the EK cleavage site).

[0041] Purification of BACE1. For the purification of BACE the 102 liters of conditioned media was used. During purification the activity of the enzyme was estimated at room temperature by continuously monitoring the fluorescent intensity for 5-10 min. at 420 nm (ext – 320 nm) Abz-Ser-Glu-Val-Asn-Leu-Asp-Ala-Glu-Phe-Arg-Dpa (Abz = Amino benzoic acid, Dpa = 9,10-diphenylanthracene) as the substrate. The reaction mixture contained 20 μM of substrate, different amounts of enzyme in 0.5 ml of 20 mM Tris-HCl pH 8.0 and 100 mM NaCl. The concentrated material of conditioned media(1.6 l) was applied to column (2.8 x 12 cm) containing ImmunoPure Immobilized Protein A agarose (Pierce, Il, USA) equilibrated in PBS buffer. The speed of application was 2 ml/min. The column was washed with 1 litre of PBS buffer and the BACE-Fc protein was eluted by ImmunoPure IgG Elution Buffer (Pierce, Il, USA). The fractions containing protein were immediately neutralized by 1 M Tris-HCl to pH 8.0.

[0042] The obtained protein material was treated with Enterokinase at 25°C. The ratio of BACE-Fc to Enterokinase was 3000:1 and the time of reaction was 3 hrs. The reaction was stopped by removing Enterokinase from reaction mixture by applying the protein to a column (1 x 5 cm) containing soybean trypsin inhibitor agarose (Sigma, Mo, USA) equilibrated in 20 mM Tris-HCL pH 8.0 containing 100 mM NaCl (speed was 1 ml/min). The flow through material contained BACE and cleaved Fc. Cleaved Fc was removed from BACE by flowing through a protein A column equilibrated in 20 mM Tris-HCl pH 8.0.

[0043] BACE was partially de-glycosylated using PNGase F (New England Labs., Ma, USA). 8-9 μg of PNGase was added to 1 mg of BACE and the incubation was carried at 37° C for 16 hrs. The additional 5-6 μg of PNGase was added to each mg of BACE and incubation was continued for another 4 hrs. The purified BACE was separated from PNGase by HPLC size-exclusion chromatography using 21.5 x 30 cm G-3000SW column (TosoHaas, Pa, USA) equilibrated in 20 mM tris-HCL pH 8.0 containing 200 mM NaCl. (Speed of elution was 3 ml/min). The purified BACE was concentrated and used for crystallization experiments.

[0044] N-terminal sequencing of purified BACE reveals a mixture of protein species, with the major sample having the processing domain cleaved and beginning at residue 47 (all numbering refers to full length BACE;accession code: A59090) and a minor sample which had not been cleaved beginning at residue 22. A smaller sample with sequence MTIAY was also detected.

[0045] Crystallization. The crystals were grown using the hanging drop vapour diffusion method. The protein was concentrated to mg/ml in 20mM Tris pH 7.5, 200mM sodium chloride. Inhibitor peptide sequence is SEVNStaVAEF, where Sta is the rare amino acid (*S*)-Statine. It was concentrated to 100mM in 100% DMSO and mixed with concentrated protein in a two-fold peptide excess to form the complex. 1 μl of complex was added to 1 μl of well solution containing 100mM Sodium Cacodylate pH6.5, 25% PEG8K, 300mM lithium sulphate. Plate-like crystal clusters grew within one week to dimensions of 20O

μm x 400 μm x 75 μm. Single crystals were transferred to a stabilizing, cryoprotectant solution which contained the well solution plus 25% Glycerol for a brief, 10 second, soak and then frozen in liquid nitrogen. X-ray diffraction crystals had space group I222, and unit cell parameters a=86.627, b=130.861, c=130.729, and $\alpha = \beta = \gamma = 90°$.

B. Results

[0046] Structure Determination and Overall Fold. Full length BACE was expressed in CHO cells as a fc fusion protein and, after purification, cleavage and partial deglycosylation, complexed with peptide inhibitor and crystallized. Crystals diffracted to 2.3Å and the structure was solved using the technique of molecular replacement. The search model used was derived from cod atlantic Pepsin and contained 63% of the final number of atoms. The density modified maps obtained using a poly-alanine version of the search model (39% of the final atoms) provided sufficient information to build all but 12 amino acids. The final model contains residues from 59 to 448 (using full length numbering), all 9 residues of the statine inhibitor and 360 water molecules. Of the four predicted N-linked glycosylation sites only two have interpretable electron density.

[0047] The overall shape of the BACE protein is spherical and is composed of two distinct domains, an N-terminal (58-207) and a C-terminal (208-447). With the first thirteen amino acids (58-71) being packed against residues 238-243. There is a significant cleft-like channel across one surface of the interface between the domains. This contains the inhibitor peptide and conserved aspartic acid motifs that define the active sites of aspartic proteases.

[0048] The N-terminal domain is composed of a single a-helix preceeding the loop joining the two domains and thirteen β-strands. The larger C-terminal domain has a total of seventeen β-strands and three α-helices. The overall topology is characterised by an eight stranded antiparallel interdomain β-sheet. This central sheet comprises the majority of the active site residues including the two conserved aspartates (one from each domain:93 and 289). Asp93 and

Asp289 define the position of a pseudo two-fold axis for the central β-sheet. Outside of this symmetry the two domains differ significantly. The N-terminal domain has an extra two strands extending the central sheet. In addition, there are two anti-parallel β-sheets above and below the central sheet composed of three and four β-strands respectively. Residues from the upper sheet (131-135) fold over the active site aspartates and form a 'flap' over the centre of the peptide binding cleft.

[0049] The C-terminal domain contains two lobes in addition to the strands which from the central β-sheet. These are weakly homologous to known aspartic protease structures. The binding pocket for the P1` and P3` positions are instead derived from three β-turns 388-391, 284-286 and 255-261.

[0050] There are a total of six cysteine residues in BACE. Each of these is involved in a disulphide interaction. The pattern of disulphide crosslinking, Cys278-Cys443, Cys380-Cys330, Cys420-Cys216 are unique in the aspartic proteases known to date.

[0051] A novel aspartic protease. The first attempts to study the relationship of function to structure of an Apartic proteases began in the 1930s with Pepsin. Since then this rich field of research has been successfully applied to the design of clinically used inhibitors in only one system; HIV protease. The reasons for this are related more to the validity of the pharmacological target than the efficacy of inhibitors. β-secretase has been described as a novel protease and has been shown to be linked to the onset and progression of Alzheimer's disease.

[0052] From a gross viewpoint the overall fold and domain organization is very similar to that of a canonical aspartic protease. The comparison at a more detailed level reveals a significant number of differences. The active site is characterized by two aspartic residues surrounded by a conserved set of hydrogen bonds termed a 'fireman's grip'. This is reproduced in the -secretase structure presented here. The characteristic flap which wraps over the active site in pepsin is absent from the C-terminal domain in a manner analogous to

cathepsin D. In β-secretase the critical main chain amide hydrogen bond to the carboxyl group of statine is maintained by Thr133 from this flap. The amide of the statine makes a hydrogen bond to the carboxyl group of Gly95, emphasizing that the statine residue occupies both the P1 and P1` position.

[0053] Enzyme Mechanism. It has been shown that β-secretase cleavage is dependent on proximity to the cell membrane. Both β-secretase and its substrate APP have putative transmembrane regions. Our expressed BACE construct finishes one amino acid before the predicted transmembrane region. The final residue in the current structure is Ile447, thirteen residues away from the beginning of the putative transmembrane domain. In the current crystal structure Ile447 is only 6Å away from the P3 Glutamic acid of the inhibitor suggesting a role for the remaining C-terminal residues in the enzyme mechanism. The Statine residue of the inhibitor peptide is bound at the S1 position within the active site. The position of the C-3 hydroxyl group, coplanar to and within hydrogen bonding distance of both aspartate 93 and 289 carboxyl groups, confirms that the rare amino acid mimics the tetrahedral transition state i.e the intermediate of peptide-bond hydrolysis. The distance between the oxygen atoms of Asp93 and Asp289 is 2.8Å, strongly suggesting a shared proton atom and a classic aspartic protease pK profile for these side-chains and a common enzyme mechanism to other known aspartic proteases.

[0054] Inhibitor binding. The inhibitor peptide binds in an extended form along a 20Å groove formed at the interface between the domains. The conserved catalytic aspartic residues lie at the middle of this groove. The bound peptide consists of 8 amino acids plus a statine amino acid at position 5. There is contiguous electron density for the whole peptide. The statine based inhibitor used in this study has been show to inhibit the β-secretase enzyme with nanomolar efficiency. The peptide sequence is based on the P10 to P4` APP751 Sweedish family mutation. This mutation of a Lys-Asn at the P2 position and Met-Leu at the P1 position is strongly correlated to the early onset of

Alzheimer's disease. The inhibitor peptide utilizes Statine's Leucyl like side-chain to explore this interaction. Due to the di-peptide nature of Satine the P1` position of the substrate is shifted to P2` leaving an empty S1` pocket. The β-secretase enzyme appears to have a novel preference for an apartate or glutamate at the P1` position whereas other aspartic proteases show a preference for hydrophobic residues. This unusual preference for a negatively charged P1' amino acid is explained by the guanadinium group of Arg189 forming part of the putative S1` pocket. Even at the acidic pH optima of BACE the arginine side chain would form a positively charged environment for the possibly protonated carboxyl side-chain atoms.

[0055] The S1 and S3 binding pockets are a contiguous, hydrophobic pocket formed by the side-chain of residues Tyr132, Phe169, Ile171, Trp176, Ile179 and main chain atoms of Gly74, and Gln73. This packing of inhibitor P1 and P3 side chains has been seen in previous aspartic protease complexes.

[0056] The canonical APP cleavage site for b-secretase appears to have a preference for a small hydrophobic residues at the P2` position. The side chain of the valine residue bound in the putative S2` site of β-secretase appears to not make any significant interactions with the protein, its main chain however forms a tight set of hydrogen bonds to the backbone carboxyl of Gly 95 and the sidechain OH of Tyr259. In turn, Tyr259 is held rigidly in place by an edge-pi interaction with Trp258, which packs against the guanadinium group of Arg256.

[0057] *Swedish mutation. Autosomal dominant mutations identified on* the β-amyloid precusor protein have been correlated to early-onset cases of Alzheimer's disease. These have been shown to cluster around the three canonical cleavage sites. A double (the so-called Swedish) mutation of Lys670-Met671 (770aa isoform of APP numbering) to Asn-Leu causes an increase in the overall quantity of Aβ detectable in the plasma and in the medium of cultured fibroblasts from carriers of the Swedish mutation. These two amino acids lie at the P2 and P1 positions of the β-secretase active site. The statine based inhibitor used here is based on this Swedish mutation. A methionine at position

P1 would clearly be accommodated but would loose the van Der Waal's complentarity exhibited by the statine side-chain to Leu90 and Ile178. The Cϵ atom of the methione would make supplement the hydrophobic interaction to Phe169.

Table 1

Residues of BACE Within 4Å of Peptide Inhibitor

SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296, ARG368

Residues of BACE Within 8Å of Peptide Inhibitor

LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396, ILE447

[0058] All publications mentioned herein above, whether to issued patents, pending applications, published articles, deposited sequences, or otherwise, are hereby incorporated by reference in their entirety. While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be appreciated by one skilled in the art from a reading of the disclosure that various changes in form and detail can be made without departing from the true scope of the invention in the appended claims.

What is claimed is:

1. A crystallized complex of Beta-site APP Cleaving Enzyme (BACE) and SER-GLU-VAL-ASN-Sta-VAL-ALA-GLU-PHE.

2. The crystallized complex of Claim 1, wherein BACE has an N-terminal domain consisting of amino acid residues 58-207 shown in Figure 1, and a C-terminal domain consisting of amino acid residues 208-447 shown in Figure 1.

3. An active site of an APP binding protein or peptide comprising the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

4. The active site of Claim 3, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

5. The active site of Claim 3, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

6. An active site of an APP binding protein or peptide comprising the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171,

ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

7. The active site of Claim 6, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

8. The active site of Claim 6, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

9. A method for identifying an agent that interacts with an active site of Beta-site APP Cleaving Enzyme (BACE), comprising the steps of:

(a) determining an active site of BACE from a three dimensional model of BACE using the relative structural coordinates of Figure 1, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) performing computer fitting analysis to identify an agent which interacts with said active site.

10. The method of Claim 9, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

11. The method of Claim 9, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

12. A method for identifying an agent that interacts with an active site of an APP binding protein or peptide, comprising the steps of:

(a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) designing an agent using the three dimensional model generated in step (a).

13. The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

14. The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

15. The method of Claim 12, wherein the agent is designed by performing computer fitting analysis of the agent with the three dimensional model generated in step (a).

16. The method of Claim 12, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

12. A method for identifying an agent that interacts with an active site of an APP binding protein or peptide, comprising the steps of:

(a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) designing an agent using the three dimensional model generated in step (a).

13. The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

14. The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

15. The method of Claim 12, wherein the agent is designed by performing computer fitting analysis of the agent with the three dimensional model generated in step (a).

16. The method of Claim 12, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

17. The method of Claim 12, wherein the APP binding protein or peptide is BACE.

18. The method of Claim 17, wherein the agent is a potential inhibitor of binding between BACE and APP.

19. The method of Claim 18, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with BACE in the presence of APP.

20. A method for identifying an agent that interacts with an active site of an APP binding protein or peptide, comprising the steps of:

(a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) designing an agent using the three dimensional model generated in step (a).

21. The method of Claim 18, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

22. The method of Claim 20, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

23. The method of Claim 20, wherein the agent is designed by performing computer fitting analysis of the agent with the three dimensional model generated in step (a).

24. The method of Claim 20, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

25. The method of Claim 20, wherein the APP binding protein or peptide is BACE.

26. The method of Claim 25, wherein the agent is a potential inhibitor of binding between BACE and APP.

27. The method of Claim 26, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with BACE in the presence of APP.

28. An agent identified by the method of Claim 9.

29. An agent identified by the method of Claim 12.

30. An agent identified by the method of Claim 20.

Figure 1

		Atom Type	Res.			X	Y	Z		
ATOM	1	N	GLY	A	58	31.563	49.775	16.324	1.00	59.33
ATOM	2	CA	GLY	A	58	32.861	50.358	16.764	1.00	58.44
ATOM	3	C	GLY	A	58	33.594	49.446	17.727	1.00	57.81
ATOM	4	O	GLY	A	58	34.067	48.331	17.333	1.00	56.66
ATOM	5	N	SER	A	59	33.712	49.888	18.975	1.00	56.66
ATOM	6	CA	SER	A	59	34.391	49.094	20.015	1.00	55.45
ATOM	7	C	SER	A	59	33.560	49.088	21.293	1.00	53.77
ATOM	8	O	SER	A	59	32.978	50.147	21.704	1.00	54.40
ATOM	9	CB	SER	A	59	35.781	49.668	20.309	1.00	55.79
ATOM	10	OG	SER	A	59	35.690	50.952	20.899	1.00	57.07
ATOM	11	N	PHE	A	60	33.480	47.924	21.927	1.00	49.96
ATOM	12	CA	PHE	A	60	32.719	47.772	23.181	1.00	45.72
ATOM	13	C	PHE	A	60	33.681	47.269	24.247	1.00	44.79
ATOM	14	O	PHE	A	60	33.495	46.160	24.831	1.00	45.45
ATOM	15	CB	PHE	A	60	31.564	46.790	22.976	1.00	43.28
ATOM	16	CG	PHE	A	60	30.557	47.249	21.957	1.00	41.00
ATOM	17	CD1	PHE	A	60	30.875	47.267	20.602	1.00	40.54
ATOM	18	CD2	PHE	A	60	29.301	47.701	22.355	1.00	40.58
ATOM	19	CE1	PHE	A	60	29.954	47.731	19.658	1.00	39.88
ATOM	20	CE2	PHE	A	60	28.375	48.166	21.419	1.00	39.50
ATOM	21	CZ	PHE	A	60	28.704	48.182	20.070	1.00	39.23
ATOM	22	N	VAL	A	61	34.709	48.073	24.500	1.00	43.29
ATOM	23	CA	VAL	A	61	35.763	47.756	25.483	1.00	43.19
ATOM	24	C	VAL	A	61	35.243	47.069	26.738	1.00	41.81
ATOM	25	O	VAL	A	61	35.876	46.099	27.247	1.00	42.54
ATOM	26	CB	VAL	A	61	36.532	49.035	25.895	1.00	43.62
ATOM	27	CG1	VAL	A	61	37.069	49.730	24.655	1.00	44.38
ATOM	28	CG2	VAL	A	61	35.621	49.975	26.676	1.00	44.28
ATOM	29	N	GLU	A	62	34.114	47.542	27.252	1.00	40.86
ATOM	30	CA	GLU	A	62	33.517	46.959	28.470	1.00	40.02
ATOM	31	C	GLU	A	62	33.208	45.473	28.320	1.00	36.45
ATOM	32	O	GLU	A	62	33.366	44.685	29.301	1.00	36.49
ATOM	33	CB	GLU	A	62	32.226	47.700	28.832	1.00	43.76
ATOM	34	CG	GLU	A	62	32.399	48.895	29.764	1.00	48.74
ATOM	35	CD	GLU	A	62	32.743	48.486	31.188	1.00	51.91
ATOM	36	OE1	GLU	A	62	32.317	47.387	31.612	1.00	53.41
ATOM	37	OE2	GLU	A	62	33.423	49.271	31.890	1.00	53.64
ATOM	38	N	MET	A	63	32.780	45.062	27.129	1.00	30.86
ATOM	39	CA	MET	A	63	32.421	43.643	26.896	1.00	27.79
ATOM	40	C	MET	A	63	33.491	42.741	26.279	1.00	26.02
ATOM	41	O	MET	A	63	33.354	41.476	26.310	1.00	25.25
ATOM	42	CB	MET	A	63	31.130	43.578	26.078	1.00	25.63
ATOM	43	CG	MET	A	63	29.942	44.133	26.858	1.00	24.89
ATOM	44	SD	MET	A	63	28.392	44.180	25.960	1.00	23.85
ATOM	45	CE	MET	A	63	28.431	45.848	25.316	1.00	24.18
ATOM	46	N	VAL	A	64	34.551	43.330	25.736	1.00	23.39
ATOM	47	CA	VAL	A	64	35.639	42.516	25.143	1.00	20.76
ATOM	48	C	VAL	A	64	36.263	41.634	26.216	1.00	20.06
ATOM	49	O	VAL	A	64	36.531	42.095	27.370	1.00	18.87
ATOM	50	CB	VAL	A	64	36.740	43.407	24.517	1.00	21.16
ATOM	51	CG1	VAL	A	64	37.958	42.567	24.151	1.00	18.99
ATOM	52	CG2	VAL	A	64	36.193	44.092	23.266	1.00	21.01
ATOM	53	N	ASP	A	65	36.487	40.373	25.869	1.00	18.21
ATOM	54	CA	ASP	A	65	37.091	39.397	26.800	1.00	18.56
ATOM	55	C	ASP	A	65	36.280	39.174	28.071	1.00	17.80
ATOM	56	O	ASP	A	65	36.869	38.964	29.165	1.00	16.29
ATOM	57	CB	ASP	A	65	38.508	39.829	27.194	1.00	21.53
ATOM	58	CG	ASP	A	65	39.409	40.055	25.993	1.00	22.65

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ATOM     59  OD1 ASP A  65      39.162  39.451  24.930  1.00 23.75
ATOM     60  OD2 ASP A  65      40.375  40.831  26.117  1.00 24.72
ATOM     61  N   ASN A  66      34.955  39.209  27.969  1.00 16.59
ATOM     62  CA  ASN A  66      34.090  38.987  29.156  1.00 16.58
ATOM     63  C   ASN A  66      33.719  37.508  29.274  1.00 17.20
ATOM     64  O   ASN A  66      32.815  37.125  30.070  1.00 19.23
ATOM     65  CB  ASN A  66      32.817  39.845  29.059  1.00 14.62
ATOM     66  CG  ASN A  66      31.967  39.516  27.835  1.00 15.57
ATOM     67  OD1 ASN A  66      32.381  38.714  26.937  1.00 16.31
ATOM     68  ND2 ASN A  66      30.788  40.120  27.760  1.00 14.85
ATOM     69  N   LEU A  67      34.409  36.664  28.515  1.00 17.73
ATOM     70  CA  LEU A  67      34.134  35.206  28.529  1.00 17.36
ATOM     71  C   LEU A  67      35.295  34.328  28.985  1.00 16.04
ATOM     72  O   LEU A  67      36.499  34.701  28.842  1.00 16.38
ATOM     73  CB  LEU A  67      33.707  34.757  27.128  1.00 17.19
ATOM     74  CG  LEU A  67      32.226  34.504  26.839  1.00 18.63
ATOM     75  CD1 LEU A  67      31.349  35.604  27.407  1.00 16.94
ATOM     76  CD2 LEU A  67      32.049  34.375  25.330  1.00 18.67
ATOM     77  N   ARG A  68      34.956  33.166  29.531  1.00 14.58
ATOM     78  CA  ARG A  68      35.961  32.173  29.973  1.00 16.73
ATOM     79  C   ARG A  68      35.394  30.775  29.717  1.00 15.78
ATOM     80  O   ARG A  68      34.154  30.610  29.500  1.00 13.85
ATOM     81  CB  ARG A  68      36.299  32.349  31.459  1.00 18.19
ATOM     82  CG  ARG A  68      37.086  33.623  31.766  1.00 21.67
ATOM     83  CD  ARG A  68      37.571  33.646  33.213  1.00 23.25
ATOM     84  NE  ARG A  68      36.462  33.653  34.165  1.00 26.34
ATOM     85  CZ  ARG A  68      36.598  33.500  35.482  1.00 27.29
ATOM     86  NH1 ARG A  68      37.802  33.324  36.015  1.00 25.91
ATOM     87  NH2 ARG A  68      35.530  33.527  36.271  1.00 26.77
ATOM     88  N   GLY A  69      36.262  29.769  29.726  1.00 14.89
ATOM     89  CA  GLY A  69      35.816  28.409  29.486  1.00 15.62
ATOM     90  C   GLY A  69      36.505  27.806  28.277  1.00 16.66
ATOM     91  O   GLY A  69      37.526  28.367  27.771  1.00 15.60
ATOM     92  N   LYS A  70      35.989  26.676  27.804  1.00 17.25
ATOM     93  CA  LYS A  70      36.556  25.973  26.629  1.00 16.95
ATOM     94  C   LYS A  70      35.472  25.138  25.949  1.00 16.87
ATOM     95  O   LYS A  70      34.394  24.864  26.562  1.00 17.19
ATOM     96  CB  LYS A  70      37.737  25.092  27.058  1.00 18.62
ATOM     97  CG  LYS A  70      37.518  24.303  28.348  1.00 19.97
ATOM     98  CD  LYS A  70      38.737  23.446  28.667  1.00 22.43
ATOM     99  CE  LYS A  70      38.538  22.611  29.926  1.00 23.77
ATOM    100  NZ  LYS A  70      39.660  21.638  30.129  1.00 22.43
ATOM    101  N   SER A  71      35.714  24.729  24.706  1.00 15.11
ATOM    102  CA  SER A  71      34.706  23.950  23.940  1.00 14.34
ATOM    103  C   SER A  71      34.155  22.730  24.667  1.00 14.36
ATOM    104  O   SER A  71      32.918  22.446  24.600  1.00 13.81
ATOM    105  CB  SER A  71      35.281  23.523  22.581  1.00 14.97
ATOM    106  OG  SER A  71      36.456  22.743  22.732  1.00 15.41
ATOM    107  N   GLY A  72      35.024  22.005  25.362  1.00 14.38
ATOM    108  CA  GLY A  72      34.588  20.815  26.072  1.00 14.63
ATOM    109  C   GLY A  72      33.661  21.022  27.262  1.00 16.49
ATOM    110  O   GLY A  72      32.772  20.159  27.537  1.00 16.20
ATOM    111  N   GLN A  73      33.814  22.129  27.979  1.00 16.78
ATOM    112  CA  GLN A  73      32.965  22.369  29.167  1.00 18.67
ATOM    113  C   GLN A  73      32.040  23.570  29.038  1.00 18.70
ATOM    114  O   GLN A  73      31.223  23.858  29.967  1.00 19.81
ATOM    115  CB  GLN A  73      33.852  22.522  30.401  1.00 20.09
ATOM    116  CG  GLN A  73      34.924  21.433  30.493  1.00 24.21
ATOM    117  CD  GLN A  73      35.624  21.400  31.837  1.00 24.83
ATOM    118  OE1 GLN A  73      36.048  22.467  32.380  1.00 26.53
ATOM    119  NE2 GLN A  73      35.769  20.206  32.395  1.00 25.73
ATOM    120  N   GLY A  74      32.138  24.274  27.914  1.00 17.65
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ATOM    121  CA  GLY A  74      31.292  25.429  27.688  1.00 15.83
ATOM    122  C   GLY A  74      31.939  26.746  28.068  1.00 15.56
ATOM    123  O   GLY A  74      32.837  26.799  28.962  1.00 17.53
ATOM    124  N   TYR A  75      31.517  27.814  27.403  1.00 13.96
ATOM    125  CA  TYR A  75      32.041  29.164  27.686  1.00 16.12
ATOM    126  C   TYR A  75      30.991  29.903  28.502  1.00 14.92
ATOM    127  O   TYR A  75      29.758  29.793  28.217  1.00 14.71
ATOM    128  CB  TYR A  75      32.324  29.918  26.385  1.00 17.79
ATOM    129  CG  TYR A  75      33.490  29.354  25.605  1.00 18.92
ATOM    130  CD1 TYR A  75      33.326  28.271  24.742  1.00 19.83
ATOM    131  CD2 TYR A  75      34.763  29.909  25.735  1.00 20.43
ATOM    132  CE1 TYR A  75      34.409  27.757  24.020  1.00 21.98
ATOM    133  CE2 TYR A  75      35.847  29.407  25.025  1.00 21.04
ATOM    134  CZ  TYR A  75      35.666  28.339  24.170  1.00 22.04
ATOM    135  OH  TYR A  75      36.746  27.882  23.456  1.00 22.86
ATOM    136  N   TYR A  76      31.432  30.653  29.507  1.00 13.66
ATOM    137  CA  TYR A  76      30.478  31.360  30.368  1.00 12.95
ATOM    138  C   TYR A  76      30.753  32.837  30.593  1.00 13.47
ATOM    139  O   TYR A  76      31.901  33.345  30.391  1.00 13.77
ATOM    140  CB  TYR A  76      30.395  30.662  31.725  1.00 13.31
ATOM    141  CG  TYR A  76      31.723  30.548  32.446  1.00 14.55
ATOM    142  CD1 TYR A  76      32.601  29.497  32.174  1.00 16.16
ATOM    143  CD2 TYR A  76      32.105  31.495  33.392  1.00 15.68
ATOM    144  CE1 TYR A  76      33.829  29.392  32.832  1.00 17.64
ATOM    145  CE2 TYR A  76      33.329  31.402  34.055  1.00 18.14
ATOM    146  CZ  TYR A  76      34.183  30.348  33.770  1.00 18.24
ATOM    147  OH  TYR A  76      35.390  30.252  34.428  1.00 21.79
ATOM    148  N   VAL A  77      29.716  33.546  31.017  1.00 12.55
ATOM    149  CA  VAL A  77      29.844  34.980  31.298  1.00 14.17
ATOM    150  C   VAL A  77      29.390  35.225  32.727  1.00 15.16
ATOM    151  O   VAL A  77      28.564  34.439  33.283  1.00 16.09
ATOM    152  CB  VAL A  77      28.975  35.821  30.336  1.00 13.43
ATOM    153  CG1 VAL A  77      27.495  35.528  30.567  1.00 11.59
ATOM    154  CG2 VAL A  77      29.281  37.305  30.524  1.00 10.74
ATOM    155  N   GLU A  78      29.905  36.276  33.352  1.00 16.88
ATOM    156  CA  GLU A  78      29.486  36.571  34.731  1.00 17.45
ATOM    157  C   GLU A  78      28.178  37.345  34.706  1.00 16.89
ATOM    158  O   GLU A  78      27.961  38.239  33.826  1.00 14.65
ATOM    159  CB  GLU A  78      30.538  37.392  35.479  1.00 19.11
ATOM    160  CG  GLU A  78      30.222  37.503  36.974  1.00 24.70
ATOM    161  CD  GLU A  78      31.225  38.342  37.757  1.00 26.24
ATOM    162  OE1 GLU A  78      31.162  39.584  37.679  1.00 27.53
ATOM    163  OE2 GLU A  78      32.076  37.755  38.452  1.00 29.49
ATOM    164  N   MET A  79      27.296  37.012  35.641  1.00 16.65
ATOM    165  CA  MET A  79      25.992  37.684  35.761  1.00 17.22
ATOM    166  C   MET A  79      25.610  37.768  37.232  1.00 17.77
ATOM    167  O   MET A  79      26.208  37.066  38.100  1.00 18.29
ATOM    168  CB  MET A  79      24.908  36.899  35.007  1.00 16.88
ATOM    169  CG  MET A  79      25.070  36.874  33.492  1.00 16.65
ATOM    170  SD  MET A  79      23.798  35.865  32.673  1.00 17.43
ATOM    171  CE  MET A  79      22.442  37.003  32.577  1.00 15.55
ATOM    172  N   THR A  80      24.637  38.617  37.539  1.00 17.73
ATOM    173  CA  THR A  80      24.146  38.741  38.917  1.00 17.50
ATOM    174  C   THR A  80      22.632  38.630  38.853  1.00 17.85
ATOM    175  O   THR A  80      21.995  39.075  37.851  1.00 17.14
ATOM    176  CB  THR A  80      24.524  40.100  39.550  1.00 18.12
ATOM    177  OG1 THR A  80      23.851  41.158  38.857  1.00 18.55
ATOM    178  CG2 THR A  80      26.031  40.328  39.474  1.00 16.48
ATOM    179  N   VAL A  81      22.042  38.020  39.874  1.00 18.24
ATOM    180  CA  VAL A  81      20.573  37.882  39.959  1.00 20.23
ATOM    181  C   VAL A  81      20.145  38.274  41.375  1.00 21.18
ATOM    182  O   VAL A  81      20.929  38.093  42.362  1.00 20.31
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ATOM    183  CB  VAL A  81      20.105  36.429  39.700  1.00 20.43
ATOM    184  CG1 VAL A  81      20.566  35.959  38.334  1.00 21.49
ATOM    185  CG2 VAL A  81      20.639  35.518  40.777  1.00 21.78
ATOM    186  N   GLY A  82      18.938  38.817  41.497  1.00 21.84
ATOM    187  CA  GLY A  82      18.421  39.200  42.799  1.00 21.10
ATOM    188  C   GLY A  82      18.973  40.475  43.404  1.00 21.47
ATOM    189  O   GLY A  82      19.864  41.159  42.814  1.00 21.97
ATOM    190  N   SER A  83      18.454  40.808  44.581  1.00 22.27
ATOM    191  CA  SER A  83      18.869  42.012  45.335  1.00 22.02
ATOM    192  C   SER A  83      18.996  41.607  46.795  1.00 20.16
ATOM    193  O   SER A  83      18.002  41.120  47.410  1.00 20.07
ATOM    194  CB  SER A  83      17.804  43.104  45.213  1.00 21.98
ATOM    195  OG  SER A  83      17.356  43.229  43.874  1.00 23.70
ATOM    196  N   PRO A  84      20.198  41.734  47.380  1.00 21.14
ATOM    197  CA  PRO A  84      21.454  42.221  46.785  1.00 20.45
ATOM    198  C   PRO A  84      21.911  41.288  45.656  1.00 20.37
ATOM    199  O   PRO A  84      21.508  40.086  45.606  1.00 18.46
ATOM    200  CB  PRO A  84      22.434  42.193  47.962  1.00 19.74
ATOM    201  CG  PRO A  84      21.548  42.320  49.166  1.00 20.71
ATOM    202  CD  PRO A  84      20.377  41.447  48.815  1.00 19.44
ATOM    203  N   PRO A  85      22.754  41.790  44.741  1.00 20.53
ATOM    204  CA  PRO A  85      23.258  40.997  43.616  1.00 20.58
ATOM    205  C   PRO A  85      23.949  39.706  44.046  1.00 20.81
ATOM    206  O   PRO A  85      24.854  39.720  44.936  1.00 21.15
ATOM    207  CB  PRO A  85      24.240  41.947  42.932  1.00 20.87
ATOM    208  CG  PRO A  85      23.732  43.294  43.282  1.00 22.23
ATOM    209  CD  PRO A  85      23.340  43.141  44.724  1.00 21.41
ATOM    210  N   GLN A  86      23.541  38.590  43.453  1.00 20.05
ATOM    211  CA  GLN A  86      24.174  37.289  43.752  1.00 19.63
ATOM    212  C   GLN A  86      24.904  36.923  42.472  1.00 20.50
ATOM    213  O   GLN A  86      24.263  36.622  41.412  1.00 19.85
ATOM    214  CB  GLN A  86      23.127  36.227  44.097  1.00 19.82
ATOM    215  CG  GLN A  86      22.283  36.586  45.314  1.00 18.97
ATOM    216  CD  GLN A  86      21.292  35.506  45.693  1.00 19.84
ATOM    217  OE1 GLN A  86      20.226  35.801  46.316  1.00 21.21
ATOM    218  NE2 GLN A  86      21.603  34.259  45.354  1.00 17.54
ATOM    219  N   THR A  87      26.229  36.969  42.527  1.00 19.61
ATOM    220  CA  THR A  87      27.057  36.669  41.346  1.00 19.61
ATOM    221  C   THR A  87      27.088  35.188  40.994  1.00 18.63
ATOM    222  O   THR A  87      27.220  34.302  41.892  1.00 18.56
ATOM    223  CB  THR A  87      28.501  37.164  41.549  1.00 19.88
ATOM    224  OG1 THR A  87      28.486  38.558  41.887  1.00 20.57
ATOM    225  CG2 THR A  87      29.304  36.977  40.278  1.00 18.65
ATOM    226  N   LEU A  88      26.972  34.907  39.701  1.00 18.38
ATOM    227  CA  LEU A  88      26.991  33.522  39.193  1.00 18.18
ATOM    228  C   LEU A  88      27.572  33.496  37.781  1.00 18.11
ATOM    229  O   LEU A  88      27.353  34.457  36.974  1.00 18.86
ATOM    230  CB  LEU A  88      25.568  32.952  39.159  1.00 16.21
ATOM    231  CG  LEU A  88      24.825  32.828  40.495  1.00 18.20
ATOM    232  CD1 LEU A  88      23.366  32.474  40.226  1.00 18.10
ATOM    233  CD2 LEU A  88      25.484  31.766  41.379  1.00 16.56
ATOM    234  N   ASN A  89      28.317  32.443  37.459  1.00 15.84
ATOM    235  CA  ASN A  89      28.876  32.312  36.101  1.00 16.22
ATOM    236  C   ASN A  89      27.841  31.544  35.300  1.00 16.03
ATOM    237  O   ASN A  89      27.363  30.450  35.735  1.00 15.05
ATOM    238  CB  ASN A  89      30.208  31.565  36.114  1.00 15.71
ATOM    239  CG  ASN A  89      31.324  32.396  36.700  1.00 16.10
ATOM    240  OD1 ASN A  89      31.390  33.650  36.477  1.00 15.48
ATOM    241  ND2 ASN A  89      32.217  31.750  37.439  1.00 14.07
ATOM    242  N   ILE A  90      27.485  32.091  34.145  1.00 15.55
ATOM    243  CA  ILE A  90      26.445  31.494  33.292  1.00 14.59
ATOM    244  C   ILE A  90      26.960  31.052  31.930  1.00 15.07
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ATOM    245  O   ILE A  90      27.578  31.867  31.173  1.00 13.01
ATOM    246  CB  ILE A  90      25.301  32.512  33.084  1.00 14.44
ATOM    247  CG1 ILE A  90      24.884  33.098  34.437  1.00 14.15
ATOM    248  CG2 ILE A  90      24.114  31.847  32.407  1.00 14.29
ATOM    249  CD1 ILE A  90      24.356  32.062  35.426  1.00 13.44
ATOM    250  N   LEU A  91      26.714  29.790  31.590  1.00 15.08
ATOM    251  CA  LEU A  91      27.153  29.249  30.284  1.00 15.63
ATOM    252  C   LEU A  91      26.313  29.878  29.174  1.00 16.04
ATOM    253  O   LEU A  91      25.041  29.904  29.250  1.00 16.72
ATOM    254  CB  LEU A  91      27.008  27.721  30.265  1.00 14.67
ATOM    255  CG  LEU A  91      27.450  26.945  29.012  1.00 15.49
ATOM    256  CD1 LEU A  91      27.692  25.485  29.364  1.00 15.10
ATOM    257  CD2 LEU A  91      26.393  27.052  27.925  1.00 15.54
ATOM    258  N   VAL A  92      26.995  30.408  28.164  1.00 16.13
ATOM    259  CA  VAL A  92      26.336  31.051  27.003  1.00 15.39
ATOM    260  C   VAL A  92      25.901  29.960  26.038  1.00 15.51
ATOM    261  O   VAL A  92      26.761  29.243  25.440  1.00 16.92
ATOM    262  CB  VAL A  92      27.306  32.008  26.278  1.00 15.40
ATOM    263  CG1 VAL A  92      26.668  32.523  24.994  1.00 16.99
ATOM    264  CG2 VAL A  92      27.671  33.172  27.200  1.00 13.64
ATOM    265  N   ASP A  93      24.594  29.824  25.845  1.00 16.41
ATOM    266  CA  ASP A  93      24.069  28.762  24.974  1.00 14.41
ATOM    267  C   ASP A  93      23.090  29.226  23.903  1.00 15.40
ATOM    268  O   ASP A  93      21.889  29.494  24.206  1.00 15.81
ATOM    269  CB  ASP A  93      23.411  27.701  25.861  1.00 16.00
ATOM    270  CG  ASP A  93      22.897  26.512  25.078  1.00 16.45
ATOM    271  OD1 ASP A  93      23.536  26.133  24.076  1.00 17.23
ATOM    272  OD2 ASP A  93      21.863  25.938  25.481  1.00 16.68
ATOM    273  N   THR A  94      23.550  29.326  22.657  1.00 13.38
ATOM    274  CA  THR A  94      22.636  29.745  21.574  1.00 13.70
ATOM    275  C   THR A  94      21.811  28.549  21.109  1.00 13.68
ATOM    276  O   THR A  94      20.941  28.671  20.190  1.00 14.18
ATOM    277  CB  THR A  94      23.397  30.349  20.362  1.00 14.99
ATOM    278  OG1 THR A  94      24.279  29.370  19.798  1.00 14.96
ATOM    279  CG2 THR A  94      24.201  31.568  20.794  1.00 14.04
ATOM    280  N   GLY A  95      22.053  27.392  21.719  1.00 14.90
ATOM    281  CA  GLY A  95      21.309  26.199  21.351  1.00 15.51
ATOM    282  C   GLY A  95      20.108  25.969  22.255  1.00 16.96
ATOM    283  O   GLY A  95      19.516  24.850  22.275  1.00 16.90
ATOM    284  N   SER A  96      19.721  26.987  23.011  1.00 17.38
ATOM    285  CA  SER A  96      18.562  26.851  23.922  1.00 17.95
ATOM    286  C   SER A  96      17.990  28.231  24.226  1.00 17.07
ATOM    287  O   SER A  96      18.573  29.269  23.803  1.00 14.94
ATOM    288  CB  SER A  96      19.005  26.174  25.219  1.00 18.55
ATOM    289  OG  SER A  96      19.640  26.894  26.276  1.00 26.99
ATOM    290  N   SER A  97      16.869  28.292  24.936  1.00 16.25
ATOM    291  CA  SER A  97      16.290  29.614  25.258  1.00 18.39
ATOM    292  C   SER A  97      15.740  29.776  26.670  1.00 17.83
ATOM    293  O   SER A  97      14.866  30.653  26.932  1.00 18.75
ATOM    294  CB  SER A  97      15.224  29.993  24.227  1.00 18.88
ATOM    295  OG  SER A  97      14.633  28.850  23.651  1.00 23.68
ATOM    296  N   ASN A  98      16.229  28.959  27.592  1.00 17.57
ATOM    297  CA  ASN A  98      15.809  29.073  28.993  1.00 16.01
ATOM    298  C   ASN A  98      16.963  29.611  29.821  1.00 16.51
ATOM    299  O   ASN A  98      18.127  29.109  29.709  1.00 16.69
ATOM    300  CB  ASN A  98      15.401  27.720  29.566  1.00 13.74
ATOM    301  CG  ASN A  98      13.969  27.359  29.241  1.00 16.04
ATOM    302  OD1 ASN A  98      13.669  26.795  28.139  1.00 13.27
ATOM    303  ND2 ASN A  98      13.058  27.680  30.158  1.00 13.26
ATOM    304  N   PHE A  99      16.688  30.640  30.614  1.00 14.45
ATOM    305  CA  PHE A  99      17.710  31.196  31.519  1.00 13.19
ATOM    306  C   PHE A  99      17.453  30.424  32.812  1.00 13.23
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ATOM    307  O   PHE A  99      16.319  30.466  33.384  1.00 11.00
ATOM    308  CB  PHE A  99      17.491  32.699  31.722  1.00 13.54
ATOM    309  CG  PHE A  99      18.390  33.318  32.761  1.00 14.79
ATOM    310  CD1 PHE A  99      19.741  32.978  32.836  1.00 15.02
ATOM    311  CD2 PHE A  99      17.889  34.258  33.657  1.00 16.17
ATOM    312  CE1 PHE A  99      20.576  33.564  33.784  1.00 14.99
ATOM    313  CE2 PHE A  99      18.718  34.852  34.610  1.00 16.36
ATOM    314  CZ  PHE A  99      20.064  34.503  34.674  1.00 14.33
ATOM    315  N   ALA A 100      18.457  29.691  33.274  1.00 11.83
ATOM    316  CA  ALA A 100      18.298  28.889  34.497  1.00 12.34
ATOM    317  C   ALA A 100      19.594  28.836  35.277  1.00 14.53
ATOM    318  O   ALA A 100      20.722  28.896  34.684  1.00 15.19
ATOM    319  CB  ALA A 100      17.849  27.486  34.138  1.00 13.09
ATOM    320  N   VAL A 101      19.467  28.727  36.595  1.00 13.51
ATOM    321  CA  VAL A 101      20.640  28.686  37.473  1.00 13.80
ATOM    322  C   VAL A 101      20.429  27.693  38.610  1.00 15.86
ATOM    323  O   VAL A 101      19.253  27.424  39.031  1.00 13.90
ATOM    324  CB  VAL A 101      20.912  30.082  38.075  1.00 14.68
ATOM    325  CG1 VAL A 101      21.126  31.098  36.962  1.00 12.49
ATOM    326  CG2 VAL A 101      19.743  30.509  38.953  1.00 13.11
ATOM    327  N   GLY A 102      21.528  27.120  39.098  1.00 16.51
ATOM    328  CA  GLY A 102      21.437  26.189  40.207  1.00 17.46
ATOM    329  C   GLY A 102      20.858  26.966  41.375  1.00 19.61
ATOM    330  O   GLY A 102      21.303  28.128  41.641  1.00 19.12
ATOM    331  N   ALA A 103      19.875  26.395  42.065  1.00 19.81
ATOM    332  CA  ALA A 103      19.241  27.092  43.212  1.00 22.41
ATOM    333  C   ALA A 103      19.098  26.169  44.414  1.00 23.71
ATOM    334  O   ALA A 103      18.196  26.366  45.293  1.00 24.50
ATOM    335  CB  ALA A 103      17.880  27.627  42.807  1.00 21.12
ATOM    336  N   ALA A 104      19.967  25.168  44.470  1.00 23.53
ATOM    337  CA  ALA A 104      19.979  24.180  45.566  1.00 24.47
ATOM    338  C   ALA A 104      21.341  23.505  45.517  1.00 24.98
ATOM    339  O   ALA A 104      21.974  23.413  44.419  1.00 26.65
ATOM    340  CB  ALA A 104      18.869  23.150  45.367  1.00 23.55
ATOM    341  N   PRO A 105      21.836  23.026  46.668  1.00 25.27
ATOM    342  CA  PRO A 105      23.140  22.361  46.733  1.00 24.87
ATOM    343  C   PRO A 105      23.328  21.286  45.672  1.00 24.16
ATOM    344  O   PRO A 105      22.350  20.594  45.251  1.00 24.35
ATOM    345  CB  PRO A 105      23.159  21.778  48.143  1.00 25.36
ATOM    346  CG  PRO A 105      22.347  22.763  48.920  1.00 25.71
ATOM    347  CD  PRO A 105      21.183  23.020  47.990  1.00 25.99
ATOM    348  N   HIS A 106      24.566  21.135  45.227  1.00 24.93
ATOM    349  CA  HIS A 106      24.918  20.119  44.223  1.00 23.63
ATOM    350  C   HIS A 106      26.402  19.843  44.367  1.00 24.29
ATOM    351  O   HIS A 106      27.207  20.790  44.596  1.00 24.19
ATOM    352  CB  HIS A 106      24.646  20.622  42.807  1.00 24.15
ATOM    353  CG  HIS A 106      24.887  19.587  41.756  1.00 24.43
ATOM    354  ND1 HIS A 106      23.912  18.702  41.348  1.00 25.53
ATOM    355  CD2 HIS A 106      26.012  19.244  41.084  1.00 23.79
ATOM    356  CE1 HIS A 106      24.426  17.857  40.471  1.00 25.66
ATOM    357  NE2 HIS A 106      25.699  18.164  40.294  1.00 24.92
ATOM    358  N   PRO A 107      26.811  18.572  44.236  1.00 25.36
ATOM    359  CA  PRO A 107      28.224  18.200  44.358  1.00 26.23
ATOM    360  C   PRO A 107      29.164  19.025  43.474  1.00 26.26
ATOM    361  O   PRO A 107      30.335  19.296  43.866  1.00 28.01
ATOM    362  CB  PRO A 107      28.225  16.722  43.972  1.00 26.21
ATOM    363  CG  PRO A 107      26.875  16.259  44.418  1.00 26.75
ATOM    364  CD  PRO A 107      25.977  17.384  43.971  1.00 25.04
ATOM    365  N   PHE A 108      28.695  19.435  42.299  1.00 25.94
ATOM    366  CA  PHE A 108      29.556  20.218  41.384  1.00 26.76
ATOM    367  C   PHE A 108      29.358  21.726  41.450  1.00 26.66
ATOM    368  O   PHE A 108      30.103  22.494  40.778  1.00 26.81
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ATOM    369  CB  PHE A 108      29.368  19.754  39.936  1.00 26.67
ATOM    370  CG  PHE A 108      29.665  18.300  39.720  1.00 26.80
ATOM    371  CD1 PHE A 108      30.531  17.614  40.569  1.00 27.67
ATOM    372  CD2 PHE A 108      29.090  17.615  38.655  1.00 27.12
ATOM    373  CE1 PHE A 108      30.819  16.262  40.359  1.00 27.99
ATOM    374  CE2 PHE A 108      29.369  16.267  38.433  1.00 26.65
ATOM    375  CZ  PHE A 108      30.235  15.587  39.286  1.00 26.94
ATOM    376  N   LEU A 109      28.386  22.180  42.231  1.00 26.14
ATOM    377  CA  LEU A 109      28.144  23.629  42.346  1.00 27.17
ATOM    378  C   LEU A 109      28.914  24.248  43.510  1.00 29.20
ATOM    379  O   LEU A 109      28.861  23.743  44.669  1.00 26.91
ATOM    380  CB  LEU A 109      26.647  23.911  42.498  1.00 25.73
ATOM    381  CG  LEU A 109      25.811  23.714  41.230  1.00 25.94
ATOM    382  CD1 LEU A 109      24.343  23.983  41.530  1.00 24.99
ATOM    383  CD2 LEU A 109      26.310  24.657  40.136  1.00 24.26
ATOM    384  N   HIS A 110      29.632  25.328  43.213  1.00 32.94
ATOM    385  CA  HIS A 110      30.442  26.077  44.207  1.00 35.82
ATOM    386  C   HIS A 110      29.533  27.015  44.983  1.00 33.93
ATOM    387  O   HIS A 110      29.732  27.265  46.209  1.00 34.20
ATOM    388  CB  HIS A 110      31.501  26.915  43.485  1.00 42.49
ATOM    389  CG  HIS A 110      32.907  26.469  43.732  1.00 47.84
ATOM    390  ND1 HIS A 110      33.509  26.558  44.969  1.00 50.74
ATOM    391  CD2 HIS A 110      33.834  25.934  42.899  1.00 49.74
ATOM    392  CE1 HIS A 110      34.746  26.098  44.888  1.00 51.83
ATOM    393  NE2 HIS A 110      34.968  25.713  43.644  1.00 51.38
ATOM    394  N   ARG A 111      28.547  27.553  44.279  1.00 31.13
ATOM    395  CA  ARG A 111      27.579  28.494  44.857  1.00 28.72
ATOM    396  C   ARG A 111      26.287  28.331  44.072  1.00 28.16
ATOM    397  O   ARG A 111      26.267  27.652  43.000  1.00 27.40
ATOM    398  CB  ARG A 111      28.108  29.924  44.717  1.00 28.09
ATOM    399  CG  ARG A 111      28.550  30.255  43.305  1.00 26.48
ATOM    400  CD  ARG A 111      29.216  31.616  43.201  1.00 25.86
ATOM    401  NE  ARG A 111      29.723  31.831  41.849  1.00 25.21
ATOM    402  CZ  ARG A 111      30.423  32.892  41.465  1.00 24.44
ATOM    403  NH1 ARG A 111      30.708  33.850  42.337  1.00 25.08
ATOM    404  NH2 ARG A 111      30.828  32.995  40.205  1.00 22.62
ATOM    405  N   TYR A 112      25.207  28.922  44.566  1.00 26.27
ATOM    406  CA  TYR A 112      23.922  28.814  43.866  1.00 23.70
ATOM    407  C   TYR A 112      22.955  29.916  44.250  1.00 22.77
ATOM    408  O   TYR A 112      23.140  30.633  45.283  1.00 21.10
ATOM    409  CB  TYR A 112      23.295  27.437  44.119  1.00 25.47
ATOM    410  CG  TYR A 112      23.036  27.111  45.575  1.00 27.20
ATOM    411  CD1 TYR A 112      21.885  27.569  46.222  1.00 28.51
ATOM    412  CD2 TYR A 112      23.946  26.353  46.309  1.00 27.51
ATOM    413  CE1 TYR A 112      21.647  27.276  47.565  1.00 27.78
ATOM    414  CE2 TYR A 112      23.720  26.058  47.651  1.00 28.63
ATOM    415  CZ  TYR A 112      22.570  26.522  48.270  1.00 28.98
ATOM    416  OH  TYR A 112      22.352  26.228  49.591  1.00 30.28
ATOM    417  N   TYR A 113      21.927  30.069  43.428  1.00 19.32
ATOM    418  CA  TYR A 113      20.896  31.090  43.624  1.00 18.94
ATOM    419  C   TYR A 113      20.047  30.807  44.857  1.00 17.90
ATOM    420  O   TYR A 113      19.480  29.688  45.011  1.00 19.37
ATOM    421  CB  TYR A 113      20.027  31.141  42.369  1.00 17.76
ATOM    422  CG  TYR A 113      18.887  32.135  42.378  1.00 17.68
ATOM    423  CD1 TYR A 113      19.024  33.397  42.963  1.00 16.86
ATOM    424  CD2 TYR A 113      17.709  31.854  41.688  1.00 16.79
ATOM    425  CE1 TYR A 113      18.020  34.349  42.848  1.00 17.05
ATOM    426  CE2 TYR A 113      16.704  32.796  41.563  1.00 16.02
ATOM    427  CZ  TYR A 113      16.858  34.038  42.138  1.00 17.36
ATOM    428  OH  TYR A 113      15.848  34.963  41.984  1.00 16.62
ATOM    429  N   GLN A 114      19.967  31.790  45.746  1.00 18.68
ATOM    430  CA  GLN A 114      19.156  31.673  46.983  1.00 20.28
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ATOM    431  C   GLN A 114      18.057  32.719  46.897  1.00 19.59
ATOM    432  O   GLN A 114      18.285  33.933  47.192  1.00 20.34
ATOM    433  CB  GLN A 114      20.028  31.912  48.216  1.00 19.79
ATOM    434  CG  GLN A 114      21.048  30.814  48.434  1.00 22.79
ATOM    435  CD  GLN A 114      21.942  31.063  49.626  1.00 24.34
ATOM    436  OE1 GLN A 114      22.708  32.073  49.668  1.00 26.47
ATOM    437  NE2 GLN A 114      21.876  30.173  50.606  1.00 24.49
ATOM    438  N   ARG A 115      16.876  32.275  46.479  1.00 20.48
ATOM    439  CA  ARG A 115      15.703  33.159  46.305  1.00 21.24
ATOM    440  C   ARG A 115      15.234  33.837  47.583  1.00 21.94
ATOM    441  O   ARG A 115      14.784  35.022  47.546  1.00 21.40
ATOM    442  CB  ARG A 115      14.550  32.366  45.686  1.00 20.21
ATOM    443  CG  ARG A 115      14.807  31.953  44.240  1.00 20.95
ATOM    444  CD  ARG A 115      13.917  30.796  43.824  1.00 20.32
ATOM    445  NE  ARG A 115      14.305  29.567  44.508  1.00 20.45
ATOM    446  CZ  ARG A 115      13.626  28.428  44.448  1.00 19.47
ATOM    447  NH1 ARG A 115      12.514  28.352  43.732  1.00 20.02
ATOM    448  NH2 ARG A 115      14.061  27.366  45.106  1.00 21.63
ATOM    449  N   GLN A 116      15.323  33.138  48.710  1.00 22.93
ATOM    450  CA  GLN A 116      14.880  33.723  49.993  1.00 24.99
ATOM    451  C   GLN A 116      15.718  34.953  50.343  1.00 23.86
ATOM    452  O   GLN A 116      15.242  35.873  51.080  1.00 24.27
ATOM    453  CB  GLN A 116      14.972  32.691  51.123  1.00 27.81
ATOM    454  CG  GLN A 116      16.391  32.280  51.502  1.00 32.89
ATOM    455  CD  GLN A 116      16.999  31.257  50.550  1.00 36.05
ATOM    456  OE1 GLN A 116      16.955  31.423  49.295  1.00 36.88
ATOM    457  NE2 GLN A 116      17.577  30.199  51.112  1.00 37.21
ATOM    458  N   LEU A 117      16.944  35.006  49.833  1.00 20.91
ATOM    459  CA  LEU A 117      17.831  36.153  50.112  1.00 20.59
ATOM    460  C   LEU A 117      17.673  37.296  49.124  1.00 19.96
ATOM    461  O   LEU A 117      18.440  38.301  49.191  1.00 18.93
ATOM    462  CB  LEU A 117      19.296  35.707  50.128  1.00 21.68
ATOM    463  CG  LEU A 117      19.887  35.224  51.454  1.00 22.49
ATOM    464  CD1 LEU A 117      19.001  34.175  52.074  1.00 22.63
ATOM    465  CD2 LEU A 117      21.286  34.675  51.210  1.00 22.12
ATOM    466  N   SER A 118      16.714  37.183  48.210  1.00 18.14
ATOM    467  CA  SER A 118      16.484  38.252  47.208  1.00 17.08
ATOM    468  C   SER A 118      15.150  38.953  47.436  1.00 16.25
ATOM    469  O   SER A 118      14.055  38.316  47.347  1.00 16.00
ATOM    470  CB  SER A 118      16.519  37.679  45.787  1.00 15.12
ATOM    471  OG  SER A 118      16.301  38.708  44.835  1.00 16.81
ATOM    472  N   SER A 119      15.210  40.250  47.711  1.00 15.31
ATOM    473  CA  SER A 119      13.991  41.044  47.973  1.00 18.09
ATOM    474  C   SER A 119      13.169  41.307  46.714  1.00 17.35
ATOM    475  O   SER A 119      11.964  41.669  46.800  1.00 17.62
ATOM    476  CB  SER A 119      14.371  42.380  48.618  1.00 16.85
ATOM    477  OG  SER A 119      15.158  43.160  47.727  1.00 18.71
ATOM    478  N   THR A 120      13.781  41.137  45.546  1.00 18.90
ATOM    479  CA  THR A 120      13.075  41.381  44.263  1.00 17.26
ATOM    480  C   THR A 120      12.587  40.104  43.594  1.00 17.17
ATOM    481  O   THR A 120      12.004  40.139  42.466  1.00 18.70
ATOM    482  CB  THR A 120      13.980  42.143  43.283  1.00 17.78
ATOM    483  OG1 THR A 120      15.305  41.609  43.355  1.00 17.35
ATOM    484  CG2 THR A 120      14.012  43.630  43.624  1.00 17.37
ATOM    485  N   TYR A 121      12.800  38.977  44.257  1.00 18.03
ATOM    486  CA  TYR A 121      12.364  37.676  43.715  1.00 18.53
ATOM    487  C   TYR A 121      10.841  37.584  43.606  1.00 18.12
ATOM    488  O   TYR A 121      10.088  38.028  44.531  1.00 19.29
ATOM    489  CB  TYR A 121      12.878  36.547  44.607  1.00 18.32
ATOM    490  CG  TYR A 121      12.187  35.225  44.368  1.00 22.03
ATOM    491  CD1 TYR A 121      12.429  34.484  43.209  1.00 21.48
ATOM    492  CD2 TYR A 121      11.268  34.725  45.291  1.00 21.95
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ATOM    493  CE1 TYR A 121      11.776  33.280  42.977  1.00 21.33
ATOM    494  CE2 TYR A 121      10.608  33.523  45.067  1.00 22.77
ATOM    495  CZ  TYR A 121      10.867  32.807  43.908  1.00 23.35
ATOM    496  OH  TYR A 121      10.206  31.622  43.682  1.00 23.63
ATOM    497  N   ARG A 122      10.365  37.039  42.492  1.00 16.86
ATOM    498  CA  ARG A 122       8.909  36.851  42.281  1.00 16.79
ATOM    499  C   ARG A 122       8.703  35.397  41.890  1.00 17.46
ATOM    500  O   ARG A 122       9.348  34.884  40.924  1.00 17.88
ATOM    501  CB  ARG A 122       8.384  37.764  41.174  1.00 14.87
ATOM    502  CG  ARG A 122       8.335  39.230  41.548  1.00 14.83
ATOM    503  CD  ARG A 122       7.895  40.067  40.369  1.00 14.98
ATOM    504  NE  ARG A 122       7.822  41.481  40.706  1.00 16.19
ATOM    505  CZ  ARG A 122       7.546  42.442  39.833  1.00 16.67
ATOM    506  NH1 ARG A 122       7.316  42.142  38.559  1.00 15.67
ATOM    507  NH2 ARG A 122       7.505  43.704  40.233  1.00 16.38
ATOM    508  N   ASP A 123       7.836  34.720  42.628  1.00 18.52
ATOM    509  CA  ASP A 123       7.538  33.296  42.388  1.00 19.00
ATOM    510  C   ASP A 123       6.435  33.147  41.347  1.00 19.87
ATOM    511  O   ASP A 123       5.342  33.757  41.490  1.00 17.59
ATOM    512  CB  ASP A 123       7.090  32.657  43.702  1.00 19.80
ATOM    513  CG  ASP A 123       6.841  31.171  43.582  1.00 20.76
ATOM    514  OD1 ASP A 123       6.933  30.615  42.463  1.00 20.41
ATOM    515  OD2 ASP A 123       6.549  30.559  44.629  1.00 22.50
ATOM    516  N   LEU A 124       6.689  32.359  40.305  1.00 20.70
ATOM    517  CA  LEU A 124       5.672  32.139  39.255  1.00 21.20
ATOM    518  C   LEU A 124       4.790  30.929  39.562  1.00 21.64
ATOM    519  O   LEU A 124       3.832  30.601  38.786  1.00 21.17
ATOM    520  CB  LEU A 124       6.343  31.978  37.888  1.00 21.51
ATOM    521  CG  LEU A 124       6.850  33.288  37.270  1.00 22.05
ATOM    522  CD1 LEU A 124       7.617  32.994  35.997  1.00 22.23
ATOM    523  CD2 LEU A 124       5.678  34.217  36.983  1.00 21.49
ATOM    524  N   ARG A 125       5.083  30.252  40.666  1.00 22.67
ATOM    525  CA  ARG A 125       4.286  29.078  41.085  1.00 25.58
ATOM    526  C   ARG A 125       4.106  28.081  39.944  1.00 26.39
ATOM    527  O   ARG A 125       2.974  27.552  39.719  1.00 26.83
ATOM    528  CB  ARG A 125       2.918  29.553  41.593  1.00 26.62
ATOM    529  CG  ARG A 125       3.016  30.511  42.783  1.00 30.02
ATOM    530  CD  ARG A 125       1.733  31.311  43.002  1.00 32.48
ATOM    531  NE  ARG A 125       1.910  32.334  44.034  1.00 36.63
ATOM    532  CZ  ARG A 125       1.049  33.323  44.282  1.00 38.12
ATOM    533  NH1 ARG A 125      -0.070  33.441  43.575  1.00 37.55
ATOM    534  NH2 ARG A 125       1.307  34.202  45.240  1.00 38.11
ATOM    535  N   LYS A 126       5.189  27.810  39.221  1.00 26.62
ATOM    536  CA  LYS A 126       5.162  26.861  38.079  1.00 26.41
ATOM    537  C   LYS A 126       6.453  26.063  37.986  1.00 24.61
ATOM    538  O   LYS A 126       7.577  26.624  38.141  1.00 22.46
ATOM    539  CB  LYS A 126       4.971  27.605  36.756  1.00 28.55
ATOM    540  CG  LYS A 126       3.539  27.804  36.326  1.00 32.76
ATOM    541  CD  LYS A 126       3.486  28.380  34.917  1.00 36.53
ATOM    542  CE  LYS A 126       2.048  28.607  34.456  1.00 38.52
ATOM    543  NZ  LYS A 126       1.234  27.355  34.550  1.00 40.78
ATOM    544  N   GLY A 127       6.326  24.770  37.731  1.00 23.25
ATOM    545  CA  GLY A 127       7.504  23.941  37.598  1.00 22.82
ATOM    546  C   GLY A 127       7.970  23.995  36.157  1.00 22.77
ATOM    547  O   GLY A 127       7.220  24.487  35.252  1.00 22.00
ATOM    548  N   VAL A 128       9.184  23.521  35.909  1.00 21.58
ATOM    549  CA  VAL A 128       9.731  23.511  34.541  1.00 22.39
ATOM    550  C   VAL A 128      10.736  22.388  34.390  1.00 21.31
ATOM    551  O   VAL A 128      11.547  22.101  35.323  1.00 21.59
ATOM    552  CB  VAL A 128      10.416  24.851  34.180  1.00 21.77
ATOM    553  CG1 VAL A 128      11.572  25.120  35.122  1.00 22.15
ATOM    554  CG2 VAL A 128      10.903  24.809  32.740  1.00 23.66
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ATOM    555  N   TYR A 129      10.700  21.744  33.233  1.00 21.64
ATOM    556  CA  TYR A 129      11.598  20.624  32.933  1.00 21.55
ATOM    557  C   TYR A 129      12.298  20.882  31.609  1.00 20.25
ATOM    558  O   TYR A 129      11.635  21.188  30.573  1.00 20.01
ATOM    559  CB  TYR A 129      10.785  19.333  32.841  1.00 23.37
ATOM    560  CG  TYR A 129      11.545  18.164  32.271  1.00 26.64
ATOM    561  CD1 TYR A 129      12.628  17.613  32.956  1.00 27.70
ATOM    562  CD2 TYR A 129      11.178  17.598  31.048  1.00 27.27
ATOM    563  CE1 TYR A 129      13.323  16.529  32.443  1.00 29.33
ATOM    564  CE2 TYR A 129      11.872  16.507  30.524  1.00 28.75
ATOM    565  CZ  TYR A 129      12.942  15.980  31.231  1.00 28.91
ATOM    566  OH  TYR A 129      13.634  14.896  30.751  1.00 30.21
ATOM    567  N   VAL A 130      13.620  20.782  31.602  1.00 19.35
ATOM    568  CA  VAL A 130      14.353  21.003  30.350  1.00 17.21
ATOM    569  C   VAL A 130      15.308  19.872  30.022  1.00 16.02
ATOM    570  O   VAL A 130      16.319  19.628  30.748  1.00 16.89
ATOM    571  CB  VAL A 130      15.136  22.334  30.370  1.00 17.86
ATOM    572  CG1 VAL A 130      15.934  22.485  29.075  1.00 15.31
ATOM    573  CG2 VAL A 130      14.163  23.505  30.525  1.00 15.67
ATOM    574  N   PRO A 131      15.013  19.136  28.945  1.00 14.83
ATOM    575  CA  PRO A 131      15.868  18.028  28.529  1.00 14.77
ATOM    576  C   PRO A 131      16.743  18.516  27.372  1.00 15.00
ATOM    577  O   PRO A 131      16.234  19.154  26.402  1.00 15.43
ATOM    578  CB  PRO A 131      14.857  16.971  28.106  1.00 13.57
ATOM    579  CG  PRO A 131      13.809  17.806  27.421  1.00 13.44
ATOM    580  CD  PRO A 131      13.706  19.078  28.262  1.00 13.99
ATOM    581  N   TYR A 132      18.043  18.268  27.465  1.00 14.75
ATOM    582  CA  TYR A 132      18.989  18.679  26.404  1.00 17.37
ATOM    583  C   TYR A 132      19.438  17.415  25.676  1.00 17.52
ATOM    584  O   TYR A 132      19.100  16.274  26.105  1.00 17.41
ATOM    585  CB  TYR A 132      20.211  19.369  27.020  1.00 16.93
ATOM    586  CG  TYR A 132      19.909  20.665  27.742  1.00 18.63
ATOM    587  CD1 TYR A 132      19.834  21.881  27.051  1.00 17.88
ATOM    588  CD2 TYR A 132      19.706  20.681  29.122  1.00 19.01
ATOM    589  CE1 TYR A 132      19.564  23.080  27.722  1.00 16.57
ATOM    590  CE2 TYR A 132      19.435  21.867  29.799  1.00 17.74
ATOM    591  CZ  TYR A 132      19.365  23.062  29.098  1.00 19.02
ATOM    592  OH  TYR A 132      19.083  24.229  29.782  1.00 18.23
ATOM    593  N   THR A 133      20.188  17.574  24.592  1.00 18.46
ATOM    594  CA  THR A 133      20.686  16.403  23.842  1.00 18.54
ATOM    595  C   THR A 133      21.525  15.580  24.812  1.00 20.42
ATOM    596  O   THR A 133      21.667  14.325  24.672  1.00 19.49
ATOM    597  CB  THR A 133      21.546  16.846  22.653  1.00 18.40
ATOM    598  OG1 THR A 133      20.720  17.539  21.708  1.00 20.46
ATOM    599  CG2 THR A 133      22.194  15.645  21.976  1.00 18.37
ATOM    600  N   GLN A 134      22.064  16.265  25.810  1.00 22.23
ATOM    601  CA  GLN A 134      22.890  15.624  26.842  1.00 24.27
ATOM    602  C   GLN A 134      22.723  16.406  28.140  1.00 23.32
ATOM    603  O   GLN A 134      23.179  17.580  28.252  1.00 21.03
ATOM    604  CB  GLN A 134      24.352  15.633  26.405  1.00 28.22
ATOM    605  CG  GLN A 134      25.140  14.412  26.808  1.00 32.76
ATOM    606  CD  GLN A 134      25.020  13.296  25.781  1.00 36.63
ATOM    607  OE1 GLN A 134      26.052  12.680  25.356  1.00 37.34
ATOM    608  NE2 GLN A 134      23.791  13.018  25.352  1.00 38.92
ATOM    609  N   GLY A 135      22.080  15.789  29.124  1.00 23.28
ATOM    610  CA  GLY A 135      21.863  16.460  30.391  1.00 21.50
ATOM    611  C   GLY A 135      20.432  16.946  30.483  1.00 22.11
ATOM    612  O   GLY A 135      19.735  17.111  29.435  1.00 20.68
ATOM    613  N   LYS A 136      19.968  17.190  31.703  1.00 22.97
ATOM    614  CA  LYS A 136      18.584  17.654  31.923  1.00 23.80
ATOM    615  C   LYS A 136      18.429  18.147  33.353  1.00 22.33
ATOM    616  O   LYS A 136      19.196  17.719  34.269  1.00 21.42
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ATOM    617  CB  LYS A 136      17.606  16.501  31.677  1.00 25.37
ATOM    618  CG  LYS A 136      17.823  15.310  32.607  1.00 28.29
ATOM    619  CD  LYS A 136      16.804  14.196  32.374  1.00 31.54
ATOM    620  CE  LYS A 136      16.955  13.570  31.000  1.00 34.21
ATOM    621  NZ  LYS A 136      15.996  12.444  30.789  1.00 37.76
ATOM    622  N   TRP A 137      17.470  19.040  33.573  1.00 21.02
ATOM    623  CA  TRP A 137      17.214  19.562  34.928  1.00 20.75
ATOM    624  C   TRP A 137      15.750  19.907  35.133  1.00 20.62
ATOM    625  O   TRP A 137      14.951  19.978  34.153  1.00 20.05
ATOM    626  CB  TRP A 137      18.077  20.800  35.231  1.00 18.46
ATOM    627  CG  TRP A 137      17.960  21.937  34.248  1.00 18.02
ATOM    628  CD1 TRP A 137      18.865  22.276  33.281  1.00 18.12
ATOM    629  CD2 TRP A 137      16.881  22.879  34.134  1.00 17.27
ATOM    630  NE1 TRP A 137      18.419  23.369  32.574  1.00 17.78
ATOM    631  CE2 TRP A 137      17.204  23.758  33.074  1.00 17.40
ATOM    632  CE3 TRP A 137      15.675  23.067  34.823  1.00 17.08
ATOM    633  CZ2 TRP A 137      16.363  24.807  32.684  1.00 15.50
ATOM    634  CZ3 TRP A 137      14.836  24.113  34.434  1.00 17.23
ATOM    635  CH2 TRP A 137      15.188  24.968  33.373  1.00 17.46
ATOM    636  N   GLU A 138      15.385  20.098  36.395  1.00 21.53
ATOM    637  CA  GLU A 138      14.014  20.472  36.789  1.00 24.94
ATOM    638  C   GLU A 138      14.166  21.642  37.745  1.00 23.18
ATOM    639  O   GLU A 138      15.168  21.719  38.526  1.00 21.21
ATOM    640  CB  GLU A 138      13.320  19.320  37.515  1.00 28.46
ATOM    641  CG  GLU A 138      13.053  18.101  36.656  1.00 34.91
ATOM    642  CD  GLU A 138      12.562  16.919  37.472  1.00 37.93
ATOM    643  OE1 GLU A 138      12.175  15.897  36.864  1.00 40.28
ATOM    644  OE2 GLU A 138      12.570  17.009  38.722  1.00 40.20
ATOM    645  N   GLY A 139      13.214  22.559  37.711  1.00 22.13
ATOM    646  CA  GLY A 139      13.298  23.693  38.604  1.00 22.60
ATOM    647  C   GLY A 139      11.975  24.402  38.713  1.00 21.54
ATOM    648  O   GLY A 139      10.949  23.953  38.116  1.00 23.29
ATOM    649  N   GLU A 140      11.962  25.494  39.465  1.00 21.74
ATOM    650  CA  GLU A 140      10.733  26.284  39.648  1.00 21.81
ATOM    651  C   GLU A 140      10.900  27.646  38.998  1.00 19.04
ATOM    652  O   GLU A 140      11.975  28.304  39.125  1.00 18.42
ATOM    653  CB  GLU A 140      10.404  26.425  41.139  1.00 24.39
ATOM    654  CG  GLU A 140      11.479  25.887  42.065  1.00 28.61
ATOM    655  CD  GLU A 140      10.922  25.385  43.383  1.00 29.72
ATOM    656  OE1 GLU A 140      10.311  24.297  43.389  1.00 31.43
ATOM    657  OE2 GLU A 140      11.091  26.077  44.410  1.00 30.48
ATOM    658  N   LEU A 141       9.870  28.071  38.278  1.00 16.35
ATOM    659  CA  LEU A 141       9.901  29.360  37.585  1.00 15.48
ATOM    660  C   LEU A 141       9.674  30.546  38.511  1.00 15.68
ATOM    661  O   LEU A 141       8.832  30.499  39.466  1.00 13.45
ATOM    662  CB  LEU A 141       8.864  29.376  36.460  1.00 15.23
ATOM    663  CG  LEU A 141       9.145  28.412  35.300  1.00 16.27
ATOM    664  CD1 LEU A 141       8.008  28.461  34.300  1.00 15.60
ATOM    665  CD2 LEU A 141      10.458  28.785  34.627  1.00 16.48
ATOM    666  N   GLY A 142      10.424  31.608  38.241  1.00 15.15
ATOM    667  CA  GLY A 142      10.323  32.819  39.015  1.00 12.33
ATOM    668  C   GLY A 142      10.845  33.953  38.167  1.00 14.67
ATOM    669  O   GLY A 142      11.242  33.758  36.971  1.00 13.75
ATOM    670  N   THR A 143      10.877  35.137  38.754  1.00 14.88
ATOM    671  CA  THR A 143      11.354  36.324  38.050  1.00 15.26
ATOM    672  C   THR A 143      12.262  37.103  39.008  1.00 14.53
ATOM    673  O   THR A 143      12.119  36.991  40.269  1.00 13.46
ATOM    674  CB  THR A 143      10.131  37.154  37.600  1.00 16.18
ATOM    675  OG1 THR A 143      10.192  37.362  36.187  1.00 20.69
ATOM    676  CG2 THR A 143      10.058  38.465  38.325  1.00 12.43
ATOM    677  N   ASP A 144      13.202  37.866  38.466  1.00 14.22
ATOM    678  CA  ASP A 144      14.117  38.652  39.321  1.00 15.38
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ATOM    679  C   ASP A 144      14.942  39.609  38.479  1.00 15.67
ATOM    680  O   ASP A 144      14.984  39.496  37.208  1.00 16.83
ATOM    681  CB  ASP A 144      15.063  37.721  40.086  1.00 15.20
ATOM    682  CG  ASP A 144      15.367  38.218  41.496  1.00 17.84
ATOM    683  OD1 ASP A 144      15.359  39.447  41.724  1.00 16.62
ATOM    684  OD2 ASP A 144      15.630  37.373  42.379  1.00 16.33
ATOM    685  N   LEU A 145      15.596  40.551  39.147  1.00 16.74
ATOM    686  CA  LEU A 145      16.442  41.537  38.454  1.00 18.66
ATOM    687  C   LEU A 145      17.757  40.854  38.101  1.00 20.21
ATOM    688  O   LEU A 145      18.381  40.147  38.961  1.00 21.75
ATOM    689  CB  LEU A 145      16.697  42.746  39.351  1.00 18.43
ATOM    690  CG  LEU A 145      15.452  43.522  39.786  1.00 19.69
ATOM    691  CD1 LEU A 145      15.878  44.720  40.628  1.00 19.11
ATOM    692  CD2 LEU A 145      14.660  43.971  38.557  1.00 18.50
ATOM    693  N   VAL A 146      18.186  41.030  36.858  1.00 20.48
ATOM    694  CA  VAL A 146      19.426  40.402  36.387  1.00 21.21
ATOM    695  C   VAL A 146      20.331  41.426  35.725  1.00 22.80
ATOM    696  O   VAL A 146      19.849  42.386  35.045  1.00 22.16
ATOM    697  CB  VAL A 146      19.118  39.265  35.373  1.00 20.39
ATOM    698  CG1 VAL A 146      20.405  38.575  34.941  1.00 20.39
ATOM    699  CG2 VAL A 146      18.163  38.261  35.998  1.00 17.90
ATOM    700  N   SER A 147      21.633  41.251  35.913  1.00 22.35
ATOM    701  CA  SER A 147      22.615  42.158  35.309  1.00 23.39
ATOM    702  C   SER A 147      23.829  41.383  34.833  1.00 21.77
ATOM    703  O   SER A 147      24.119  40.242  35.321  1.00 20.08
ATOM    704  CB  SER A 147      23.059  43.225  36.316  1.00 25.41
ATOM    705  OG  SER A 147      21.993  44.107  36.627  1.00 31.97
ATOM    706  N   ILE A 148      24.534  41.972  33.878  1.00 19.69
ATOM    707  CA  ILE A 148      25.757  41.377  33.329  1.00 19.14
ATOM    708  C   ILE A 148      26.853  42.405  33.614  1.00 18.85
ATOM    709  O   ILE A 148      27.021  43.408  32.853  1.00 17.87
ATOM    710  CB  ILE A 148      25.618  41.137  31.817  1.00 18.61
ATOM    711  CG1 ILE A 148      24.449  40.181  31.559  1.00 19.01
ATOM    712  CG2 ILE A 148      26.909  40.564  31.255  1.00 17.68
ATOM    713  CD1 ILE A 148      24.221  39.864  30.097  1.00 19.61
ATOM    714  N   PRO A 149      27.601  42.214  34.711  1.00 17.99
ATOM    715  CA  PRO A 149      28.679  43.134  35.095  1.00 21.17
ATOM    716  C   PRO A 149      29.523  43.638  33.926  1.00 22.18
ATOM    717  O   PRO A 149      29.800  44.869  33.823  1.00 24.08
ATOM    718  CB  PRO A 149      29.485  42.317  36.103  1.00 19.87
ATOM    719  CG  PRO A 149      28.404  41.529  36.797  1.00 19.57
ATOM    720  CD  PRO A 149      27.542  41.061  35.628  1.00 17.55
ATOM    721  N   HIS A 150      29.930  42.733  33.041  1.00 23.43
ATOM    722  CA  HIS A 150      30.748  43.119  31.869  1.00 23.84
ATOM    723  C   HIS A 150      29.933  43.067  30.588  1.00 24.47
ATOM    724  O   HIS A 150      30.334  42.431  29.566  1.00 25.89
ATOM    725  CB  HIS A 150      31.968  42.211  31.765  1.00 23.54
ATOM    726  CG  HIS A 150      32.880  42.313  32.945  1.00 26.15
ATOM    727  ND1 HIS A 150      33.619  43.446  33.216  1.00 27.28
ATOM    728  CD2 HIS A 150      33.149  41.439  33.943  1.00 26.32
ATOM    729  CE1 HIS A 150      34.305  43.264  34.330  1.00 27.48
ATOM    730  NE2 HIS A 150      34.038  42.055  34.791  1.00 28.01
ATOM    731  N   GLY A 151      28.785  43.727  30.630  1.00 25.49
ATOM    732  CA  GLY A 151      27.906  43.784  29.485  1.00 26.41
ATOM    733  C   GLY A 151      27.325  45.179  29.468  1.00 27.16
ATOM    734  O   GLY A 151      27.981  46.136  29.983  1.00 26.97
ATOM    735  N   PRO A 152      26.125  45.370  28.903  1.00 28.12
ATOM    736  CA  PRO A 152      25.540  46.712  28.880  1.00 28.75
ATOM    737  C   PRO A 152      25.219  47.165  30.304  1.00 30.53
ATOM    738  O   PRO A 152      24.844  46.331  31.182  1.00 28.62
ATOM    739  CB  PRO A 152      24.294  46.528  28.017  1.00 29.49
ATOM    740  CG  PRO A 152      23.897  45.105  28.303  1.00 29.85
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ATOM    741  CD  PRO A 152      25.227  44.385  28.277  1.00 28.15
ATOM    742  N   ASN A 153      25.375  48.457  30.560  1.00 33.03
ATOM    743  CA  ASN A 153      25.111  49.016  31.902  1.00 34.39
ATOM    744  C   ASN A 153      23.604  49.096  32.144  1.00 33.81
ATOM    745  O   ASN A 153      23.009  50.218  32.222  1.00 33.63
ATOM    746  CB  ASN A 153      25.755  50.401  32.009  1.00 37.16
ATOM    747  CG  ASN A 153      25.680  50.978  33.406  1.00 38.88
ATOM    748  OD1 ASN A 153      25.974  50.272  34.416  1.00 40.17
ATOM    749  ND2 ASN A 153      25.309  52.251  33.504  1.00 39.91
ATOM    750  N   VAL A 154      22.971  47.934  32.265  1.00 31.55
ATOM    751  CA  VAL A 154      21.514  47.872  32.486  1.00 29.59
ATOM    752  C   VAL A 154      21.113  46.739  33.418  1.00 29.47
ATOM    753  O   VAL A 154      21.924  45.809  33.718  1.00 30.24
ATOM    754  CB  VAL A 154      20.755  47.681  31.154  1.00 29.95
ATOM    755  CG1 VAL A 154      20.990  48.875  30.242  1.00 29.70
ATOM    756  CG2 VAL A 154      21.216  46.397  30.474  1.00 28.94
ATOM    757  N   THR A 155      19.874  46.799  33.882  1.00 27.83
ATOM    758  CA  THR A 155      19.323  45.773  34.779  1.00 27.61
ATOM    759  C   THR A 155      17.918  45.472  34.296  1.00 26.01
ATOM    760  O   THR A 155      17.114  46.413  34.041  1.00 27.70
ATOM    761  CB  THR A 155      19.268  46.280  36.229  1.00 27.24
ATOM    762  OG1 THR A 155      20.603  46.486  36.703  1.00 29.54
ATOM    763  CG2 THR A 155      18.573  45.270  37.129  1.00 27.37
ATOM    764  N   VAL A 156      17.592  44.197  34.143  1.00 24.69
ATOM    765  CA  VAL A 156      16.241  43.847  33.672  1.00 24.32
ATOM    766  C   VAL A 156      15.631  42.736  34.504  1.00 23.23
ATOM    767  O   VAL A 156      16.364  41.920  35.154  1.00 23.57
ATOM    768  CB  VAL A 156      16.253  43.402  32.184  1.00 25.34
ATOM    769  CG1 VAL A 156      17.178  44.302  31.379  1.00 26.63
ATOM    770  CG2 VAL A 156      16.684  41.960  32.063  1.00 24.89
ATOM    771  N   ARG A 157      14.306  42.687  34.521  1.00 21.44
ATOM    772  CA  ARG A 157      13.613  41.626  35.262  1.00 20.90
ATOM    773  C   ARG A 157      13.374  40.560  34.215  1.00 20.13
ATOM    774  O   ARG A 157      12.746  40.836  33.152  1.00 19.99
ATOM    775  CB  ARG A 157      12.280  42.121  35.830  1.00 20.03
ATOM    776  CG  ARG A 157      11.528  41.053  36.621  1.00 18.95
ATOM    777  CD  ARG A 157      10.271  41.616  37.260  1.00 18.99
ATOM    778  NE  ARG A 157      10.554  42.408  38.456  1.00 18.47
ATOM    779  CZ  ARG A 157      10.973  41.902  39.613  1.00 19.19
ATOM    780  NH1 ARG A 157      11.167  40.596  39.747  1.00 18.30
ATOM    781  NH2 ARG A 157      11.178  42.703  40.650  1.00 15.82
ATOM    782  N   ALA A 158      13.878  39.359  34.463  1.00 20.27
ATOM    783  CA  ALA A 158      13.713  38.266  33.496  1.00 19.08
ATOM    784  C   ALA A 158      13.279  36.986  34.175  1.00 19.45
ATOM    785  O   ALA A 158      13.379  36.845  35.432  1.00 19.64
ATOM    786  CB  ALA A 158      15.017  38.031  32.756  1.00 18.56
ATOM    787  N   ASN A 159      12.792  36.053  33.370  1.00 18.08
ATOM    788  CA  ASN A 159      12.363  34.756  33.876  1.00 18.21
ATOM    789  C   ASN A 159      13.607  33.992  34.282  1.00 18.60
ATOM    790  O   ASN A 159      14.666  34.033  33.577  1.00 19.42
ATOM    791  CB  ASN A 159      11.601  33.992  32.797  1.00 16.91
ATOM    792  CG  ASN A 159      10.282  34.647  32.459  1.00 18.46
ATOM    793  OD1 ASN A 159       9.479  34.978  33.381  1.00 19.46
ATOM    794  ND2 ASN A 159      10.020  34.848  31.174  1.00 16.51
ATOM    795  N   ILE A 160      13.518  33.311  35.412  1.00 18.73
ATOM    796  CA  ILE A 160      14.643  32.529  35.916  1.00 17.64
ATOM    797  C   ILE A 160      14.112  31.191  36.373  1.00 19.09
ATOM    798  O   ILE A 160      13.122  31.125  37.176  1.00 18.38
ATOM    799  CB  ILE A 160      15.319  33.212  37.128  1.00 18.36
ATOM    800  CG1 ILE A 160      15.764  34.629  36.758  1.00 17.90
ATOM    801  CG2 ILE A 160      16.521  32.394  37.585  1.00 17.16
ATOM    802  CD1 ILE A 160      16.521  35.336  37.875  1.00 18.56
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ATOM	803	N	ALA	A	161	14.717	30.123	35.871	1.00 17.55
ATOM	804	CA	ALA	A	161	14.314	28.778	36.275	1.00 18.11
ATOM	805	C	ALA	A	161	15.267	28.394	37.399	1.00 18.26
ATOM	806	O	ALA	A	161	16.507	28.223	37.166	1.00 17.61
ATOM	807	CB	ALA	A	161	14.447	27.805	35.105	1.00 17.28
ATOM	808	N	ALA	A	162	14.737	28.283	38.614	1.00 17.99
ATOM	809	CA	ALA	A	162	15.567	27.901	39.775	1.00 18.02
ATOM	810	C	ALA	A	162	15.746	26.382	39.774	1.00 18.52
ATOM	811	O	ALA	A	162	14.835	25.619	40.207	1.00 18.43
ATOM	812	CB	ALA	A	162	14.897	28.359	41.067	1.00 17.36
ATOM	813	N	ILE	A	163	16.900	25.928	39.300	1.00 19.89
ATOM	814	CA	ILE	A	163	17.204	24.480	39.215	1.00 18.56
ATOM	815	C	ILE	A	163	17.314	23.802	40.577	1.00 20.34
ATOM	816	O	ILE	A	163	18.238	24.122	41.402	1.00 19.83
ATOM	817	CB	ILE	A	163	18.512	24.245	38.430	1.00 17.19
ATOM	818	CG1	ILE	A	163	18.347	24.753	36.994	1.00 16.02
ATOM	819	CG2	ILE	A	163	18.874	22.761	38.445	1.00 14.93
ATOM	820	CD1	ILE	A	163	19.628	24.735	36.174	1.00 16.24
ATOM	821	N	THR	A	164	16.409	22.860	40.826	1.00 20.42
ATOM	822	CA	THR	A	164	16.379	22.122	42.112	1.00 23.01
ATOM	823	C	THR	A	164	16.817	20.665	41.958	1.00 24.30
ATOM	824	O	THR	A	164	17.119	19.966	42.973	1.00 26.25
ATOM	825	CB	THR	A	164	14.966	22.173	42.735	1.00 22.01
ATOM	826	OG1	THR	A	164	13.990	21.799	41.754	1.00 22.15
ATOM	827	CG2	THR	A	164	14.656	23.584	43.214	1.00 22.73
ATOM	828	N	GLU	A	165	16.858	20.187	40.721	1.00 25.84
ATOM	829	CA	GLU	A	165	17.281	18.804	40.444	1.00 27.82
ATOM	830	C	GLU	A	165	17.800	18.693	39.024	1.00 26.80
ATOM	831	O	GLU	A	165	17.246	19.323	38.072	1.00 26.59
ATOM	832	CB	GLU	A	165	16.121	17.834	40.678	1.00 31.67
ATOM	833	CG	GLU	A	165	16.233	17.118	42.020	1.00 38.94
ATOM	834	CD	GLU	A	165	14.913	16.568	42.519	1.00 41.54
ATOM	835	OE1	GLU	A	165	14.282	15.765	41.796	1.00 44.35
ATOM	836	OE2	GLU	A	165	14.510	16.940	43.644	1.00 43.84
ATOM	837	N	SER	A	166	18.861	17.919	38.852	1.00 24.81
ATOM	838	CA	SER	A	166	19.455	17.765	37.525	1.00 25.32
ATOM	839	C	SER	A	166	20.213	16.459	37.397	1.00 25.44
ATOM	840	O	SER	A	166	20.551	15.795	38.427	1.00 24.00
ATOM	841	CB	SER	A	166	20.405	18.928	37.255	1.00 23.13
ATOM	842	OG	SER	A	166	21.444	18.939	38.217	1.00 21.22
ATOM	843	N	ASP	A	167	20.490	16.079	36.155	1.00 26.01
ATOM	844	CA	ASP	A	167	21.227	14.842	35.871	1.00 26.62
ATOM	845	C	ASP	A	167	22.138	15.038	34.671	1.00 25.62
ATOM	846	O	ASP	A	167	21.656	15.300	33.528	1.00 24.35
ATOM	847	CB	ASP	A	167	20.253	13.691	35.601	1.00 30.53
ATOM	848	CG	ASP	A	167	20.966	12.370	35.387	1.00 32.67
ATOM	849	OD1	ASP	A	167	21.912	12.083	36.152	1.00 36.14
ATOM	850	OD2	ASP	A	167	20.586	11.615	34.469	1.00 34.63
ATOM	851	N	LYS	A	168	23.440	14.930	34.910	1.00 25.32
ATOM	852	CA	LYS	A	168	24.461	15.078	33.847	1.00 25.94
ATOM	853	C	LYS	A	168	24.416	16.445	33.175	1.00 25.49
ATOM	854	O	LYS	A	168	24.742	16.580	31.955	1.00 25.50
ATOM	855	CB	LYS	A	168	24.282	13.979	32.800	1.00 27.68
ATOM	856	CG	LYS	A	168	24.408	12.570	33.362	1.00 30.33
ATOM	857	CD	LYS	A	168	24.117	11.532	32.292	1.00 32.36
ATOM	858	CE	LYS	A	168	24.205	10.126	32.855	1.00 34.37
ATOM	859	NZ	LYS	A	168	23.889	9.101	31.821	1.00 36.50
ATOM	860	N	PHE	A	169	24.024	17.460	33.937	1.00 22.87
ATOM	861	CA	PHE	A	169	23.942	18.835	33.418	1.00 20.96
ATOM	862	C	PHE	A	169	25.158	19.616	33.897	1.00 22.06
ATOM	863	O	PHE	A	169	25.983	20.119	33.069	1.00 20.71
ATOM	864	CB	PHE	A	169	22.668	19.506	33.919	1.00 19.76

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ATOM    865  CG  PHE A 169      22.526  20.931  33.479  1.00 18.95
ATOM    866  CD1 PHE A 169      22.400  21.248  32.130  1.00 18.27
ATOM    867  CD2 PHE A 169      22.525  21.963  34.416  1.00 18.36
ATOM    868  CE1 PHE A 169      22.275  22.571  31.720  1.00 16.94
ATOM    869  CE2 PHE A 169      22.401  23.287  34.013  1.00 17.25
ATOM    870  CZ  PHE A 169      22.275  23.590  32.661  1.00 16.89
ATOM    871  N   PHE A 170      25.292  19.738  35.212  1.00 20.46
ATOM    872  CA  PHE A 170      26.438  20.452  35.788  1.00 21.45
ATOM    873  C   PHE A 170      27.702  19.620  35.574  1.00 22.40
ATOM    874  O   PHE A 170      27.675  18.355  35.665  1.00 22.55
ATOM    875  CB  PHE A 170      26.205  20.705  37.281  1.00 19.44
ATOM    876  CG  PHE A 170      25.079  21.663  37.559  1.00 18.44
ATOM    877  CD1 PHE A 170      23.988  21.276  38.330  1.00 18.45
ATOM    878  CD2 PHE A 170      25.098  22.948  37.025  1.00 16.73
ATOM    879  CE1 PHE A 170      22.932  22.154  38.563  1.00 17.50
ATOM    880  CE2 PHE A 170      24.046  23.832  37.253  1.00 17.78
ATOM    881  CZ  PHE A 170      22.963  23.432  38.023  1.00 16.39
ATOM    882  N   ILE A 171      28.805  20.297  35.272  1.00 23.10
ATOM    883  CA  ILE A 171      30.095  19.615  35.043  1.00 22.87
ATOM    884  C   ILE A 171      31.057  19.962  36.163  1.00 24.02
ATOM    885  O   ILE A 171      31.222  21.162  36.537  1.00 22.48
ATOM    886  CB  ILE A 171      30.729  20.048  33.704  1.00 24.70
ATOM    887  CG1 ILE A 171      29.823  19.632  32.544  1.00 22.57
ATOM    888  CG2 ILE A 171      32.123  19.434  33.558  1.00 22.35
ATOM    889  CD1 ILE A 171      30.319  20.100  31.192  1.00 23.46
ATOM    890  N   ASN A 172      31.702  18.942  36.709  1.00 27.12
ATOM    891  CA  ASN A 172      32.657  19.143  37.809  1.00 30.01
ATOM    892  C   ASN A 172      33.864  19.975  37.359  1.00 29.57
ATOM    893  O   ASN A 172      34.616  19.574  36.418  1.00 29.20
ATOM    894  CB  ASN A 172      33.105  17.779  38.337  1.00 31.92
ATOM    895  CG  ASN A 172      33.913  17.885  39.608  1.00 34.74
ATOM    896  OD1 ASN A 172      33.615  18.737  40.504  1.00 36.04
ATOM    897  ND2 ASN A 172      34.927  17.034  39.734  1.00 36.14
ATOM    898  N   GLY A 173      34.049  21.132  37.991  1.00 28.24
ATOM    899  CA  GLY A 173      35.166  22.001  37.659  1.00 27.99
ATOM    900  C   GLY A 173      34.973  22.938  36.476  1.00 28.87
ATOM    901  O   GLY A 173      35.944  23.644  36.063  1.00 29.20
ATOM    902  N   SER A 174      33.769  22.988  35.914  1.00 28.95
ATOM    903  CA  SER A 174      33.498  23.880  34.748  1.00 29.13
ATOM    904  C   SER A 174      33.524  25.348  35.168  1.00 27.92
ATOM    905  O   SER A 174      33.878  26.255  34.354  1.00 29.51
ATOM    906  CB  SER A 174      32.130  23.562  34.148  1.00 28.90
ATOM    907  OG  SER A 174      31.102  23.922  35.054  1.00 30.49
ATOM    908  N   ASN A 175      33.140  25.593  36.416  1.00 25.45
ATOM    909  CA  ASN A 175      33.095  26.951  37.011  1.00 23.59
ATOM    910  C   ASN A 175      31.855  27.767  36.647  1.00 21.71
ATOM    911  O   ASN A 175      31.828  29.019  36.853  1.00 20.11
ATOM    912  CB  ASN A 175      34.354  27.754  36.662  1.00 27.01
ATOM    913  CG  ASN A 175      34.548  28.950  37.582  1.00 29.09
ATOM    914  OD1 ASN A 175      34.648  28.794  38.840  1.00 30.19
ATOM    915  ND2 ASN A 175      34.600  30.144  37.004  1.00 30.01
ATOM    916  N   TRP A 176      30.841  27.121  36.078  1.00 16.70
ATOM    917  CA  TRP A 176      29.590  27.847  35.790  1.00 18.41
ATOM    918  C   TRP A 176      28.482  27.170  36.580  1.00 17.87
ATOM    919  O   TRP A 176      28.534  25.927  36.838  1.00 15.45
ATOM    920  CB  TRP A 176      29.248  27.888  34.292  1.00 16.48
ATOM    921  CG  TRP A 176      29.257  26.588  33.563  1.00 17.63
ATOM    922  CD1 TRP A 176      30.291  26.063  32.842  1.00 17.33
ATOM    923  CD2 TRP A 176      28.165  25.668  33.425  1.00 17.78
ATOM    924  NE1 TRP A 176      29.911  24.881  32.258  1.00 16.01
ATOM    925  CE2 TRP A 176      28.612  24.613  32.599  1.00 16.95
ATOM    926  CE3 TRP A 176      26.852  25.635  33.918  1.00 18.29
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ATOM    927  CZ2 TRP A 176      27.794  23.532  32.252  1.00 17.40
ATOM    928  CZ3 TRP A 176      26.034  24.557  33.573  1.00 19.02
ATOM    929  CH2 TRP A 176      26.512  23.521  32.747  1.00 19.06
ATOM    930  N   GLU A 177      27.496  27.950  37.005  1.00 18.68
ATOM    931  CA  GLU A 177      26.387  27.385  37.797  1.00 21.01
ATOM    932  C   GLU A 177      25.024  27.700  37.224  1.00 20.81
ATOM    933  O   GLU A 177      23.977  27.582  37.938  1.00 21.08
ATOM    934  CB  GLU A 177      26.461  27.869  39.250  1.00 22.84
ATOM    935  CG  GLU A 177      26.865  29.322  39.443  1.00 26.63
ATOM    936  CD  GLU A 177      28.377  29.531  39.446  1.00 27.90
ATOM    937  OE1 GLU A 177      29.121  28.568  39.726  1.00 28.44
ATOM    938  OE2 GLU A 177      28.818  30.670  39.186  1.00 28.24
ATOM    939  N   GLY A 178      25.007  28.088  35.953  1.00 18.48
ATOM    940  CA  GLY A 178      23.759  28.411  35.295  1.00 16.82
ATOM    941  C   GLY A 178      23.929  28.406  33.791  1.00 15.90
ATOM    942  O   GLY A 178      25.070  28.248  33.264  1.00 15.75
ATOM    943  N   ILE A 179      22.831  28.589  33.076  1.00 14.53
ATOM    944  CA  ILE A 179      22.882  28.588  31.610  1.00 14.26
ATOM    945  C   ILE A 179      22.007  29.701  31.057  1.00 14.53
ATOM    946  O   ILE A 179      20.896  29.980  31.603  1.00 15.23
ATOM    947  CB  ILE A 179      22.428  27.217  31.069  1.00 14.45
ATOM    948  CG1 ILE A 179      22.535  27.183  29.548  1.00 14.28
ATOM    949  CG2 ILE A 179      21.002  26.921  31.525  1.00 13.41
ATOM    950  CD1 ILE A 179      22.359  25.788  28.974  1.00 13.85
ATOM    951  N   LEU A 180      22.489  30.350  29.998  1.00 14.91
ATOM    952  CA  LEU A 180      21.763  31.464  29.353  1.00 14.24
ATOM    953  C   LEU A 180      21.311  31.050  27.961  1.00 15.19
ATOM    954  O   LEU A 180      22.117  31.115  26.973  1.00 15.79
ATOM    955  CB  LEU A 180      22.675  32.690  29.223  1.00 14.83
ATOM    956  CG  LEU A 180      22.078  34.107  29.257  1.00 16.59
ATOM    957  CD1 LEU A 180      22.902  34.996  28.351  1.00 15.04
ATOM    958  CD2 LEU A 180      20.622  34.120  28.818  1.00 17.08
ATOM    959  N   GLY A 181      20.057  30.621  27.851  1.00 15.40
ATOM    960  CA  GLY A 181      19.525  30.227  26.561  1.00 13.68
ATOM    961  C   GLY A 181      19.276  31.481  25.741  1.00 15.03
ATOM    962  O   GLY A 181      18.402  32.330  26.107  1.00 14.58
ATOM    963  N   LEU A 182      20.002  31.629  24.638  1.00 12.84
ATOM    964  CA  LEU A 182      19.859  32.831  23.787  1.00 13.53
ATOM    965  C   LEU A 182      19.029  32.646  22.521  1.00 14.25
ATOM    966  O   LEU A 182      18.883  33.607  21.701  1.00 13.52
ATOM    967  CB  LEU A 182      21.250  33.352  23.418  1.00 13.44
ATOM    968  CG  LEU A 182      22.036  33.949  24.583  1.00 11.84
ATOM    969  CD1 LEU A 182      23.506  34.067  24.211  1.00 11.17
ATOM    970  CD2 LEU A 182      21.450  35.311  24.936  1.00 12.14
ATOM    971  N   ALA A 183      18.491  31.449  22.322  1.00 15.12
ATOM    972  CA  ALA A 183      17.660  31.183  21.131  1.00 15.16
ATOM    973  C   ALA A 183      16.276  31.788  21.361  1.00 17.66
ATOM    974  O   ALA A 183      16.053  32.526  22.377  1.00 16.26
ATOM    975  CB  ALA A 183      17.557  29.684  20.875  1.00 14.23
ATOM    976  N   TYR A 184      15.338  31.487  20.466  1.00 18.41
ATOM    977  CA  TYR A 184      13.976  32.060  20.550  1.00 17.40
ATOM    978  C   TYR A 184      12.953  31.334  21.424  1.00 18.41
ATOM    979  O   TYR A 184      13.131  30.135  21.807  1.00 14.95
ATOM    980  CB  TYR A 184      13.411  32.237  19.138  1.00 18.07
ATOM    981  CG  TYR A 184      14.327  33.017  18.216  1.00 19.50
ATOM    982  CD1 TYR A 184      15.295  32.367  17.446  1.00 19.23
ATOM    983  CD2 TYR A 184      14.233  34.408  18.119  1.00 19.65
ATOM    984  CE1 TYR A 184      16.144  33.083  16.599  1.00 19.22
ATOM    985  CE2 TYR A 184      15.079  35.134  17.279  1.00 19.50
ATOM    986  CZ  TYR A 184      16.027  34.466  16.521  1.00 19.86
ATOM    987  OH  TYR A 184      16.842  35.185  15.670  1.00 20.69
ATOM    988  N   ALA A 185      11.873  32.046  21.734  1.00 16.29
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ATOM    989  CA  ALA A 185      10.784  31.519  22.592  1.00 17.90
ATOM    990  C   ALA A 185      10.185  30.221  22.068  1.00 17.38
ATOM    991  O   ALA A 185       9.682  29.372  22.869  1.00 15.41
ATOM    992  CB  ALA A 185       9.690  32.579  22.742  1.00 15.99
ATOM    993  N   GLU A 186      10.232  30.046  20.751  1.00 20.56
ATOM    994  CA  GLU A 186       9.679  28.846  20.086  1.00 23.43
ATOM    995  C   GLU A 186      10.169  27.533  20.690  1.00 23.87
ATOM    996  O   GLU A 186       9.448  26.486  20.619  1.00 24.67
ATOM    997  CB  GLU A 186      10.009  28.887  18.591  1.00 27.60
ATOM    998  CG  GLU A 186       9.447  27.729  17.786  1.00 32.42
ATOM    999  CD  GLU A 186       7.941  27.593  17.923  1.00 36.08
ATOM   1000  OE1 GLU A 186       7.255  28.633  18.041  1.00 39.03
ATOM   1001  OE2 GLU A 186       7.439  26.448  17.900  1.00 37.05
ATOM   1002  N   ILE A 187      11.363  27.540  21.283  1.00 22.31
ATOM   1003  CA  ILE A 187      11.904  26.302  21.900  1.00 19.35
ATOM   1004  C   ILE A 187      12.113  26.441  23.403  1.00 20.13
ATOM   1005  O   ILE A 187      12.887  25.654  24.034  1.00 19.35
ATOM   1006  CB  ILE A 187      13.241  25.872  21.248  1.00 19.03
ATOM   1007  CG1 ILE A 187      14.270  26.998  21.355  1.00 18.36
ATOM   1008  CG2 ILE A 187      13.008  25.488  19.795  1.00 19.03
ATOM   1009  CD1 ILE A 187      15.627  26.635  20.780  1.00 17.45
ATOM   1010  N   ALA A 188      11.441  27.416  23.999  1.00 19.82
ATOM   1011  CA  ALA A 188      11.551  27.636  25.454  1.00 20.35
ATOM   1012  C   ALA A 188      10.622  26.661  26.171  1.00 19.60
ATOM   1013  O   ALA A 188       9.554  26.277  25.618  1.00 19.52
ATOM   1014  CB  ALA A 188      11.160  29.083  25.793  1.00 17.16
ATOM   1015  N   ARG A 189      11.004  26.231  27.372  1.00 20.77
ATOM   1016  CA  ARG A 189      10.142  25.324  28.164  1.00 21.43
ATOM   1017  C   ARG A 189       9.577  26.162  29.303  1.00 22.80
ATOM   1018  O   ARG A 189      10.274  27.099  29.817  1.00 23.68
ATOM   1019  CB  ARG A 189      10.949  24.151  28.753  1.00 22.36
ATOM   1020  CG  ARG A 189      11.689  23.285  27.729  1.00 23.90
ATOM   1021  CD  ARG A 189      10.765  22.818  26.624  1.00 24.33
ATOM   1022  NE  ARG A 189      11.419  21.914  25.681  1.00 25.35
ATOM   1023  CZ  ARG A 189      11.336  20.586  25.724  1.00 27.35
ATOM   1024  NH1 ARG A 189      10.620  19.991  26.673  1.00 24.73
ATOM   1025  NH2 ARG A 189      11.959  19.849  24.807  1.00 25.42
ATOM   1026  N   PRO A 190       8.325  25.890  29.725  1.00 23.27
ATOM   1027  CA  PRO A 190       7.442  24.830  29.216  1.00 23.21
ATOM   1028  C   PRO A 190       6.826  25.110  27.849  1.00 23.72
ATOM   1029  O   PRO A 190       6.458  24.157  27.101  1.00 23.77
ATOM   1030  CB  PRO A 190       6.377  24.713  30.305  1.00 22.63
ATOM   1031  CG  PRO A 190       6.285  26.115  30.830  1.00 24.33
ATOM   1032  CD  PRO A 190       7.745  26.527  30.921  1.00 22.73
ATOM   1033  N   ASP A 191       6.681  26.383  27.508  1.00 25.20
ATOM   1034  CA  ASP A 191       6.107  26.754  26.202  1.00 25.89
ATOM   1035  C   ASP A 191       6.653  28.106  25.770  1.00 25.76
ATOM   1036  O   ASP A 191       7.488  28.716  26.498  1.00 24.40
ATOM   1037  CB  ASP A 191       4.569  26.757  26.269  1.00 28.36
ATOM   1038  CG  ASP A 191       4.024  27.697  27.323  1.00 30.16
ATOM   1039  OD1 ASP A 191       2.887  27.468  27.783  1.00 33.88
ATOM   1040  OD2 ASP A 191       4.714  28.669  27.686  1.00 30.53
ATOM   1041  N   ASP A 192       6.214  28.596  24.617  1.00 26.01
ATOM   1042  CA  ASP A 192       6.724  29.877  24.088  1.00 26.22
ATOM   1043  C   ASP A 192       6.236  31.123  24.813  1.00 26.52
ATOM   1044  O   ASP A 192       6.567  32.275  24.395  1.00 26.27
ATOM   1045  CB  ASP A 192       6.419  29.985  22.589  1.00 27.69
ATOM   1046  CG  ASP A 192       4.940  30.161  22.296  1.00 29.61
ATOM   1047  OD1 ASP A 192       4.102  29.647  23.066  1.00 31.87
ATOM   1048  OD2 ASP A 192       4.618  30.805  21.279  1.00 30.31
ATOM   1049  N   SER A 193       5.470  30.947  25.885  1.00 24.46
ATOM   1050  CA  SER A 193       4.988  32.117  26.645  1.00 24.21
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ATOM   1051  C   SER A 193       6.078  32.565  27.614  1.00 22.68
ATOM   1052  O   SER A 193       6.082  33.740  28.082  1.00 22.41
ATOM   1053  CB  SER A 193       3.701  31.787  27.415  1.00 25.67
ATOM   1054  OG  SER A 193       3.910  30.774  28.386  1.00 27.13
ATOM   1055  N   LEU A 194       7.009  31.670  27.932  1.00 20.84
ATOM   1056  CA  LEU A 194       8.107  32.044  28.852  1.00 18.87
ATOM   1057  C   LEU A 194       9.149  32.830  28.065  1.00 18.82
ATOM   1058  O   LEU A 194      10.066  32.240  27.419  1.00 19.19
ATOM   1059  CB  LEU A 194       8.758  30.809  29.469  1.00 17.48
ATOM   1060  CG  LEU A 194       9.680  31.201  30.631  1.00 19.18
ATOM   1061  CD1 LEU A 194       8.825  31.633  31.825  1.00 16.80
ATOM   1062  CD2 LEU A 194      10.585  30.044  31.014  1.00 16.32
ATOM   1063  N   GLU A 195       9.025  34.150  28.095  1.00 18.44
ATOM   1064  CA  GLU A 195       9.949  35.029  27.369  1.00 18.80
ATOM   1065  C   GLU A 195      11.415  34.777  27.733  1.00 19.02
ATOM   1066  O   GLU A 195      11.791  34.754  28.953  1.00 17.72
ATOM   1067  CB  GLU A 195       9.575  36.485  27.644  1.00 20.83
ATOM   1068  CG  GLU A 195      10.514  37.512  27.047  1.00 23.03
ATOM   1069  CD  GLU A 195       9.989  38.926  27.204  1.00 24.10
ATOM   1070  OE1 GLU A 195       9.211  39.373  26.337  1.00 25.77
ATOM   1071  OE2 GLU A 195      10.343  39.585  28.203  1.00 24.06
ATOM   1072  N   PRO A 196      12.272  34.559  26.714  1.00 18.43
ATOM   1073  CA  PRO A 196      13.702  34.311  26.935  1.00 18.17
ATOM   1074  C   PRO A 196      14.385  35.571  27.447  1.00 16.90
ATOM   1075  O   PRO A 196      13.845  36.715  27.297  1.00 17.67
ATOM   1076  CB  PRO A 196      14.210  33.914  25.546  1.00 17.79
ATOM   1077  CG  PRO A 196      12.992  33.305  24.892  1.00 19.11
ATOM   1078  CD  PRO A 196      11.911  34.287  25.310  1.00 18.58
ATOM   1079  N   PHE A 197      15.558  35.405  28.039  1.00 15.80
ATOM   1080  CA  PHE A 197      16.290  36.550  28.574  1.00 14.47
ATOM   1081  C   PHE A 197      16.597  37.663  27.576  1.00 16.31
ATOM   1082  O   PHE A 197      16.392  38.873  27.894  1.00 14.87
ATOM   1083  CB  PHE A 197      17.595  36.093  29.217  1.00 12.99
ATOM   1084  CG  PHE A 197      18.472  37.227  29.652  1.00 13.09
ATOM   1085  CD1 PHE A 197      19.376  37.806  28.767  1.00 12.33
ATOM   1086  CD2 PHE A 197      18.347  37.766  30.926  1.00 14.29
ATOM   1087  CE1 PHE A 197      20.139  38.907  29.143  1.00 12.22
ATOM   1088  CE2 PHE A 197      19.108  38.873  31.310  1.00 14.64
ATOM   1089  CZ  PHE A 197      20.002  39.441  30.415  1.00 13.26
ATOM   1090  N   PHE A 198      17.089  37.319  26.390  1.00 16.71
ATOM   1091  CA  PHE A 198      17.427  38.384  25.431  1.00 17.60
ATOM   1092  C   PHE A 198      16.212  39.192  25.001  1.00 17.52
ATOM   1093  O   PHE A 198      16.317  40.434  24.774  1.00 16.03
ATOM   1094  CB  PHE A 198      18.133  37.829  24.196  1.00 17.77
ATOM   1095  CG  PHE A 198      19.051  38.826  23.549  1.00 17.92
ATOM   1096  CD1 PHE A 198      20.310  39.075  24.087  1.00 18.66
ATOM   1097  CD2 PHE A 198      18.633  39.569  22.455  1.00 16.90
ATOM   1098  CE1 PHE A 198      21.139  40.053  23.546  1.00 18.55
ATOM   1099  CE2 PHE A 198      19.454  40.551  21.904  1.00 17.96
ATOM   1100  CZ  PHE A 198      20.708  40.795  22.451  1.00 18.52
ATOM   1101  N   ASP A 199      15.066  38.530  24.879  1.00 17.52
ATOM   1102  CA  ASP A 199      13.819  39.225  24.491  1.00 19.54
ATOM   1103  C   ASP A 199      13.464  40.261  25.561  1.00 18.83
ATOM   1104  O   ASP A 199      13.134  41.444  25.233  1.00 20.48
ATOM   1105  CB  ASP A 199      12.685  38.210  24.338  1.00 21.95
ATOM   1106  CG  ASP A 199      12.868  37.312  23.126  1.00 24.77
ATOM   1107  OD1 ASP A 199      12.408  37.687  22.028  1.00 27.27
ATOM   1108  OD2 ASP A 199      13.481  36.234  23.261  1.00 27.11
ATOM   1109  N   SER A 200      13.530  39.858  26.829  1.00 17.89
ATOM   1110  CA  SER A 200      13.223  40.784  27.947  1.00 16.17
ATOM   1111  C   SER A 200      14.211  41.943  27.915  1.00 16.77
ATOM   1112  O   SER A 200      13.823  43.140  28.072  1.00 17.20
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ATOM   1113  CB  SER A 200      13.336  40.062  29.292  1.00 14.55
ATOM   1114  OG  SER A 200      12.386  39.017  29.400  1.00 14.16
ATOM   1115  N   LEU A 201      15.481  41.617  27.711  1.00 16.47
ATOM   1116  CA  LEU A 201      16.553  42.638  27.654  1.00 18.93
ATOM   1117  C   LEU A 201      16.237  43.684  26.586  1.00 18.88
ATOM   1118  O   LEU A 201      16.274  44.917  26.852  1.00 18.26
ATOM   1119  CB  LEU A 201      17.884  41.953  27.337  1.00 18.68
ATOM   1120  CG  LEU A 201      19.244  42.637  27.523  1.00 20.59
ATOM   1121  CD1 LEU A 201      19.973  42.616  26.194  1.00 20.98
ATOM   1122  CD2 LEU A 201      19.100  44.053  28.045  1.00 20.13
ATOM   1123  N   VAL A 202      15.919  43.222  25.383  1.00 20.38
ATOM   1124  CA  VAL A 202      15.600  44.130  24.264  1.00 20.23
ATOM   1125  C   VAL A 202      14.335  44.938  24.532  1.00 23.13
ATOM   1126  O   VAL A 202      14.284  46.175  24.255  1.00 23.36
ATOM   1127  CB  VAL A 202      15.433  43.337  22.948  1.00 19.84
ATOM   1128  CG1 VAL A 202      14.830  44.228  21.855  1.00 17.60
ATOM   1129  CG2 VAL A 202      16.792  42.804  22.502  1.00 16.36
ATOM   1130  N   LYS A 203      13.315  44.285  25.074  1.00 24.15
ATOM   1131  CA  LYS A 203      12.050  44.985  25.360  1.00 27.77
ATOM   1132  C   LYS A 203      12.178  46.049  26.452  1.00 27.47
ATOM   1133  O   LYS A 203      11.753  47.223  26.252  1.00 26.63
ATOM   1134  CB  LYS A 203      10.970  43.973  25.746  1.00 29.55
ATOM   1135  CG  LYS A 203       9.609  44.594  26.008  1.00 34.08
ATOM   1136  CD  LYS A 203       8.497  43.798  25.335  1.00 36.82
ATOM   1137  CE  LYS A 203       8.504  42.342  25.774  1.00 38.97
ATOM   1138  NZ  LYS A 203       7.512  41.533  25.012  1.00 40.86
ATOM   1139  N   GLN A 204      12.771  45.687  27.585  1.00 26.46
ATOM   1140  CA  GLN A 204      12.910  46.632  28.721  1.00 26.94
ATOM   1141  C   GLN A 204      14.125  47.542  28.614  1.00 28.51
ATOM   1142  O   GLN A 204      14.479  48.264  29.600  1.00 30.36
ATOM   1143  CB  GLN A 204      13.007  45.848  30.032  1.00 24.17
ATOM   1144  CG  GLN A 204      11.980  44.739  30.170  1.00 20.78
ATOM   1145  CD  GLN A 204      12.270  43.821  31.342  1.00 20.14
ATOM   1146  OE1 GLN A 204      11.725  42.676  31.420  1.00 19.72
ATOM   1147  NE2 GLN A 204      13.107  44.279  32.265  1.00 16.56
ATOM   1148  N   THR A 205      14.762  47.568  27.453  1.00 28.58
ATOM   1149  CA  THR A 205      15.979  48.375  27.306  1.00 29.06
ATOM   1150  C   THR A 205      16.186  48.905  25.885  1.00 30.58
ATOM   1151  O   THR A 205      15.427  48.525  24.940  1.00 30.23
ATOM   1152  CB  THR A 205      17.175  47.501  27.772  1.00 29.85
ATOM   1153  OG1 THR A 205      17.572  47.899  29.088  1.00 29.62
ATOM   1154  CG2 THR A 205      18.328  47.576  26.823  1.00 29.03
ATOM   1155  N   HIS A 206      17.175  49.784  25.711  1.00 31.92
ATOM   1156  CA  HIS A 206      17.488  50.350  24.372  1.00 33.38
ATOM   1157  C   HIS A 206      18.548  49.530  23.637  1.00 32.31
ATOM   1158  O   HIS A 206      18.905  49.845  22.460  1.00 31.08
ATOM   1159  CB  HIS A 206      17.975  51.799  24.487  1.00 36.39
ATOM   1160  CG  HIS A 206      16.898  52.773  24.848  1.00 39.92
ATOM   1161  ND1 HIS A 206      15.696  52.836  24.177  1.00 40.95
ATOM   1162  CD2 HIS A 206      16.849  53.736  25.800  1.00 40.35
ATOM   1163  CE1 HIS A 206      14.951  53.794  24.699  1.00 41.58
ATOM   1164  NE2 HIS A 206      15.627  54.356  25.685  1.00 41.65
ATOM   1165  N   VAL A 207      19.075  48.501  24.291  1.00 29.55
ATOM   1166  CA  VAL A 207      20.097  47.639  23.651  1.00 28.49
ATOM   1167  C   VAL A 207      19.511  47.083  22.354  1.00 26.27
ATOM   1168  O   VAL A 207      18.415  46.441  22.358  1.00 26.26
ATOM   1169  CB  VAL A 207      20.498  46.462  24.572  1.00 28.77
ATOM   1170  CG1 VAL A 207      21.399  45.491  23.825  1.00 29.45
ATOM   1171  CG2 VAL A 207      21.219  46.987  25.805  1.00 28.52
ATOM   1172  N   PRO A 208      20.192  47.311  21.220  1.00 24.42
ATOM   1173  CA  PRO A 208      19.683  46.804  19.944  1.00 23.82
ATOM   1174  C   PRO A 208      19.547  45.284  19.914  1.00 22.81
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ATOM	1175	O	PRO	A	208	20.290	44.545	20.630	1.00 21.12
ATOM	1176	CB	PRO	A	208	20.689	47.343	18.926	1.00 24.65
ATOM	1177	CG	PRO	A	208	21.927	47.510	19.711	1.00 25.77
ATOM	1178	CD	PRO	A	208	21.441	48.062	21.025	1.00 24.39
ATOM	1179	N	ASN	A	209	18.605	44.806	19.109	1.00 21.59
ATOM	1180	CA	ASN	A	209	18.322	43.362	18.995	1.00 20.43
ATOM	1181	C	ASN	A	209	19.390	42.599	18.222	1.00 20.52
ATOM	1182	O	ASN	A	209	19.190	42.217	17.026	1.00 21.39
ATOM	1183	CB	ASN	A	209	16.957	43.159	18.340	1.00 18.52
ATOM	1184	CG	ASN	A	209	16.501	41.728	18.402	1.00 18.12
ATOM	1185	OD1	ASN	A	209	16.968	40.948	19.281	1.00 18.32
ATOM	1186	ND2	ASN	A	209	15.594	41.348	17.513	1.00 15.63
ATOM	1187	N	LEU	A	210	20.514	42.346	18.883	1.00 19.53
ATOM	1188	CA	LEU	A	210	21.631	41.634	18.243	1.00 19.83
ATOM	1189	C	LEU	A	210	22.765	41.421	19.226	1.00 19.02
ATOM	1190	O	LEU	A	210	22.958	42.238	20.176	1.00 18.52
ATOM	1191	CB	LEU	A	210	22.120	42.451	17.035	1.00 21.93
ATOM	1192	CG	LEU	A	210	23.534	42.305	16.456	1.00 22.75
ATOM	1193	CD1	LEU	A	210	23.612	43.009	15.102	1.00 23.20
ATOM	1194	CD2	LEU	A	210	24.548	42.910	17.409	1.00 24.60
ATOM	1195	N	PHE	A	211	23.509	40.334	19.044	1.00 16.48
ATOM	1196	CA	PHE	A	211	24.671	40.055	19.909	1.00 16.70
ATOM	1197	C	PHE	A	211	25.722	39.310	19.095	1.00 16.08
ATOM	1198	O	PHE	A	211	25.392	38.653	18.063	1.00 17.22
ATOM	1199	CB	PHE	A	211	24.251	39.280	21.173	1.00 14.67
ATOM	1200	CG	PHE	A	211	23.813	37.863	20.924	1.00 16.01
ATOM	1201	CD1	PHE	A	211	24.748	36.837	20.835	1.00 14.91
ATOM	1202	CD2	PHE	A	211	22.465	37.546	20.824	1.00 14.62
ATOM	1203	CE1	PHE	A	211	24.344	35.515	20.653	1.00 15.05
ATOM	1204	CE2	PHE	A	211	22.054	36.224	20.641	1.00 15.47
ATOM	1205	CZ	PHE	A	211	22.996	35.207	20.558	1.00 12.73
ATOM	1206	N	SER	A	212	26.977	39.424	19.520	1.00 17.19
ATOM	1207	CA	SER	A	212	28.126	38.803	18.818	1.00 16.98
ATOM	1208	C	SER	A	212	28.894	37.862	19.725	1.00 16.10
ATOM	1209	O	SER	A	212	29.036	38.122	20.955	1.00 14.22
ATOM	1210	CB	SER	A	212	29.094	39.888	18.349	1.00 16.89
ATOM	1211	OG	SER	A	212	28.431	40.869	17.593	1.00 26.70
ATOM	1212	N	LEU	A	213	29.430	36.797	19.144	1.00 14.76
ATOM	1213	CA	LEU	A	213	30.194	35.819	19.930	1.00 14.81
ATOM	1214	C	LEU	A	213	31.563	35.509	19.352	1.00 14.32
ATOM	1215	O	LEU	A	213	31.702	35.162	18.137	1.00 12.74
ATOM	1216	CB	LEU	A	213	29.394	34.522	20.060	1.00 15.67
ATOM	1217	CG	LEU	A	213	28.735	34.210	21.408	1.00 18.95
ATOM	1218	CD1	LEU	A	213	28.196	35.475	22.050	1.00 18.65
ATOM	1219	CD2	LEU	A	213	27.627	33.185	21.192	1.00 16.46
ATOM	1220	N	GLN	A	214	32.581	35.656	20.191	1.00 14.19
ATOM	1221	CA	GLN	A	214	33.954	35.324	19.797	1.00 15.89
ATOM	1222	C	GLN	A	214	34.407	34.258	20.778	1.00 15.04
ATOM	1223	O	GLN	A	214	34.848	34.582	21.917	1.00 16.01
ATOM	1224	CB	GLN	A	214	34.903	36.523	19.914	1.00 17.92
ATOM	1225	CG	GLN	A	214	36.290	36.231	19.341	1.00 20.63
ATOM	1226	CD	GLN	A	214	37.397	37.099	19.932	1.00 23.22
ATOM	1227	OE1	GLN	A	214	38.459	37.332	19.273	1.00 24.79
ATOM	1228	NE2	GLN	A	214	37.199	37.571	21.156	1.00 24.53
ATOM	1229	N	LEU	A	215	34.284	32.997	20.390	1.00 14.37
ATOM	1230	CA	LEU	A	215	34.729	31.890	21.262	1.00 13.74
ATOM	1231	C	LEU	A	215	36.193	31.625	20.925	1.00 14.40
ATOM	1232	O	LEU	A	215	36.541	31.357	19.737	1.00 14.39
ATOM	1233	CB	LEU	A	215	33.872	30.644	21.005	1.00 13.94
ATOM	1234	CG	LEU	A	215	32.636	30.429	21.893	1.00 14.78
ATOM	1235	CD1	LEU	A	215	31.900	31.734	22.143	1.00 13.31
ATOM	1236	CD2	LEU	A	215	31.723	29.407	21.240	1.00 12.97

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ATOM   1237  N   CYS A 216      37.066  31.706  21.922  1.00 14.83
ATOM   1238  CA  CYS A 216      38.504  31.486  21.682  1.00 16.37
ATOM   1239  C   CYS A 216      39.066  30.196  22.263  1.00 17.20
ATOM   1240  O   CYS A 216      39.174  30.046  23.519  1.00 16.79
ATOM   1241  CB  CYS A 216      39.314  32.668  22.227  1.00 19.03
ATOM   1242  SG  CYS A 216      38.852  34.278  21.505  1.00 23.75
ATOM   1243  N   GLY A 217      39.415  29.257  21.387  1.00 15.43
ATOM   1244  CA  GLY A 217      40.018  28.021  21.843  1.00 16.40
ATOM   1245  C   GLY A 217      41.483  28.371  22.064  1.00 17.87
ATOM   1246  O   GLY A 217      42.057  29.204  21.303  1.00 17.53
ATOM   1247  N   ALA A 218      42.119  27.785  23.069  1.00 17.79
ATOM   1248  CA  ALA A 218      43.539  28.108  23.349  1.00 16.33
ATOM   1249  C   ALA A 218      44.486  27.408  22.379  1.00 17.71
ATOM   1250  O   ALA A 218      45.602  27.927  22.069  1.00 16.46
ATOM   1251  CB  ALA A 218      43.884  27.731  24.779  1.00 14.95
ATOM   1252  N   GLY A 219      44.073  26.245  21.890  1.00 16.19
ATOM   1253  CA  GLY A 219      44.909  25.505  20.970  1.00 17.57
ATOM   1254  C   GLY A 219      45.696  24.439  21.703  1.00 17.52
ATOM   1255  O   GLY A 219      46.490  23.675  21.076  1.00 16.29
ATOM   1256  N   PHE A 220      45.502  24.375  23.018  1.00 17.13
ATOM   1257  CA  PHE A 220      46.190  23.381  23.873  1.00 18.29
ATOM   1258  C   PHE A 220      45.381  23.185  25.153  1.00 19.24
ATOM   1259  O   PHE A 220      44.477  24.012  25.475  1.00 19.69
ATOM   1260  CB  PHE A 220      47.616  23.854  24.187  1.00 18.72
ATOM   1261  CG  PHE A 220      47.689  25.253  24.731  1.00 20.07
ATOM   1262  CD1 PHE A 220      47.448  25.507  26.077  1.00 20.91
ATOM   1263  CD2 PHE A 220      47.984  26.320  23.890  1.00 19.91
ATOM   1264  CE1 PHE A 220      47.505  26.809  26.576  1.00 21.79
ATOM   1265  CE2 PHE A 220      48.043  27.620  24.374  1.00 20.35
ATOM   1266  CZ  PHE A 220      47.802  27.866  25.721  1.00 21.77
ATOM   1267  N   PRO A 221      45.659  22.110  25.907  1.00 20.17
ATOM   1268  CA  PRO A 221      44.922  21.846  27.147  1.00 21.27
ATOM   1269  C   PRO A 221      45.014  22.959  28.180  1.00 23.04
ATOM   1270  O   PRO A 221      46.065  23.666  28.292  1.00 23.99
ATOM   1271  CB  PRO A 221      45.545  20.543  27.648  1.00 20.22
ATOM   1272  CG  PRO A 221      45.946  19.855  26.390  1.00 20.63
ATOM   1273  CD  PRO A 221      46.571  20.994  25.602  1.00 20.45
ATOM   1274  N   LEU A 222      43.934  23.132  28.933  1.00 25.72
ATOM   1275  CA  LEU A 222      43.873  24.158  29.991  1.00 28.32
ATOM   1276  C   LEU A 222      43.425  23.516  31.291  1.00 30.88
ATOM   1277  O   LEU A 222      42.248  23.042  31.403  1.00 31.71
ATOM   1278  CB  LEU A 222      42.880  25.261  29.620  1.00 27.52
ATOM   1279  CG  LEU A 222      43.264  26.233  28.506  1.00 27.30
ATOM   1280  CD1 LEU A 222      42.040  27.042  28.096  1.00 26.79
ATOM   1281  CD2 LEU A 222      44.382  27.143  28.983  1.00 27.13
ATOM   1282  N   ASN A 223      44.320  23.470  32.273  1.00 34.15
ATOM   1283  CA  ASN A 223      43.959  22.893  33.583  1.00 37.64
ATOM   1284  C   ASN A 223      43.014  23.882  34.254  1.00 38.54
ATOM   1285  O   ASN A 223      42.864  25.056  33.785  1.00 36.72
ATOM   1286  CB  ASN A 223      45.204  22.663  34.457  1.00 38.54
ATOM   1287  CG  ASN A 223      45.905  23.952  34.839  1.00 39.09
ATOM   1288  OD1 ASN A 223      45.268  24.903  35.375  1.00 41.39
ATOM   1289  ND2 ASN A 223      47.208  24.013  34.595  1.00 40.09
ATOM   1290  N   GLN A 224      42.380  23.444  35.335  1.00 41.79
ATOM   1291  CA  GLN A 224      41.415  24.278  36.073  1.00 43.58
ATOM   1292  C   GLN A 224      41.898  25.708  36.359  1.00 42.52
ATOM   1293  O   GLN A 224      41.138  26.705  36.126  1.00 42.75
ATOM   1294  CB  GLN A 224      41.021  23.572  37.378  1.00 46.22
ATOM   1295  CG  GLN A 224      39.629  23.956  37.827  1.00 49.86
ATOM   1296  CD  GLN A 224      39.085  23.160  38.990  1.00 51.40
ATOM   1297  OE1 GLN A 224      37.923  23.406  39.443  1.00 52.42
ATOM   1298  NE2 GLN A 224      39.866  22.215  39.496  1.00 52.75
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ATOM   1299  N   SER A 225      43.133  25.852  36.831  1.00 40.27
ATOM   1300  CA  SER A 225      43.669  27.200  37.138  1.00 39.30
ATOM   1301  C   SER A 225      43.989  28.028  35.893  1.00 36.57
ATOM   1302  O   SER A 225      43.920  29.292  35.930  1.00 36.27
ATOM   1303  CB  SER A 225      44.917  27.094  38.027  1.00 40.27
ATOM   1304  OG  SER A 225      45.974  26.411  37.376  1.00 42.21
ATOM   1305  N   GLU A 226      44.339  27.364  34.796  1.00 34.29
ATOM   1306  CA  GLU A 226      44.654  28.083  33.542  1.00 32.79
ATOM   1307  C   GLU A 226      43.375  28.651  32.954  1.00 31.17
ATOM   1308  O   GLU A 226      43.354  29.815  32.454  1.00 29.09
ATOM   1309  CB  GLU A 226      45.307  27.144  32.526  1.00 33.69
ATOM   1310  CG  GLU A 226      46.708  26.696  32.902  1.00 36.40
ATOM   1311  CD  GLU A 226      47.251  25.619  31.972  1.00 37.70
ATOM   1312  OE1 GLU A 226      46.585  24.567  31.830  1.00 37.54
ATOM   1313  OE2 GLU A 226      48.340  25.823  31.389  1.00 37.14
ATOM   1314  N   VAL A 227      42.305  27.867  33.007  1.00 29.89
ATOM   1315  CA  VAL A 227      41.013  28.312  32.458  1.00 30.15
ATOM   1316  C   VAL A 227      40.512  29.547  33.203  1.00 29.84
ATOM   1317  O   VAL A 227      39.922  30.484  32.582  1.00 30.30
ATOM   1318  CB  VAL A 227      39.940  27.210  32.558  1.00 30.93
ATOM   1319  CG1 VAL A 227      38.800  27.538  31.637  1.00 32.67
ATOM   1320  CG2 VAL A 227      40.516  25.867  32.183  1.00 32.31
ATOM   1321  N   LEU A 228      40.731  29.581  34.513  1.00 28.88
ATOM   1322  CA  LEU A 228      40.292  30.726  35.336  1.00 27.31
ATOM   1323  C   LEU A 228      41.059  31.992  34.975  1.00 27.59
ATOM   1324  O   LEU A 228      40.491  33.129  35.020  1.00 27.84
ATOM   1325  CB  LEU A 228      40.496  30.420  36.819  1.00 27.50
ATOM   1326  CG  LEU A 228      39.700  29.259  37.419  1.00 29.32
ATOM   1327  CD1 LEU A 228      40.129  29.053  38.867  1.00 28.16
ATOM   1328  CD2 LEU A 228      38.205  29.549  37.339  1.00 28.58
ATOM   1329  N   ALA A 229      42.327  31.835  34.610  1.00 27.12
ATOM   1330  CA  ALA A 229      43.176  32.998  34.257  1.00 27.64
ATOM   1331  C   ALA A 229      43.134  33.347  32.776  1.00 27.65
ATOM   1332  O   ALA A 229      43.460  34.504  32.375  1.00 29.94
ATOM   1333  CB  ALA A 229      44.617  32.736  34.682  1.00 27.52
ATOM   1334  N   SER A 230      42.736  32.393  31.947  1.00 26.68
ATOM   1335  CA  SER A 230      42.692  32.635  30.498  1.00 26.33
ATOM   1336  C   SER A 230      41.438  33.360  30.032  1.00 26.22
ATOM   1337  O   SER A 230      40.356  33.302  30.695  1.00 25.70
ATOM   1338  CB  SER A 230      42.815  31.310  29.746  1.00 26.07
ATOM   1339  OG  SER A 230      42.759  31.519  28.344  1.00 26.54
ATOM   1340  N   VAL A 231      41.562  34.056  28.909  1.00 25.03
ATOM   1341  CA  VAL A 231      40.415  34.764  28.320  1.00 24.89
ATOM   1342  C   VAL A 231      39.785  33.776  27.346  1.00 24.75
ATOM   1343  O   VAL A 231      40.453  33.310  26.371  1.00 25.97
ATOM   1344  CB  VAL A 231      40.859  36.043  27.568  1.00 24.38
ATOM   1345  CG1 VAL A 231      39.729  36.554  26.678  1.00 22.98
ATOM   1346  CG2 VAL A 231      41.244  37.119  28.577  1.00 23.20
ATOM   1347  N   GLY A 232      38.526  33.433  27.588  1.00 23.26
ATOM   1348  CA  GLY A 232      37.846  32.481  26.729  1.00 22.77
ATOM   1349  C   GLY A 232      37.125  33.081  25.538  1.00 21.57
ATOM   1350  O   GLY A 232      36.590  32.324  24.666  1.00 20.69
ATOM   1351  N   GLY A 233      37.078  34.408  25.468  1.00 19.21
ATOM   1352  CA  GLY A 233      36.410  35.050  24.353  1.00 17.96
ATOM   1353  C   GLY A 233      35.599  36.275  24.731  1.00 18.25
ATOM   1354  O   GLY A 233      35.778  36.866  25.851  1.00 15.19
ATOM   1355  N   SER A 234      34.708  36.677  23.828  1.00 16.58
ATOM   1356  CA  SER A 234      33.864  37.864  24.053  1.00 16.83
ATOM   1357  C   SER A 234      32.423  37.667  23.599  1.00 17.82
ATOM   1358  O   SER A 234      32.134  36.995  22.552  1.00 17.90
ATOM   1359  CB  SER A 234      34.426  39.072  23.291  1.00 16.36
ATOM   1360  OG  SER A 234      35.816  39.253  23.508  1.00 18.23
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ATOM   1361  N   MET A 235      31.506  38.227  24.372  1.00 18.00
ATOM   1362  CA  MET A 235      30.091  38.201  24.010  1.00 17.58
ATOM   1363  C   MET A 235      29.732  39.677  23.996  1.00 18.27
ATOM   1364  O   MET A 235      29.594  40.322  25.087  1.00 19.03
ATOM   1365  CB  MET A 235      29.232  37.475  25.046  1.00 16.91
ATOM   1366  CG  MET A 235      27.759  37.455  24.634  1.00 17.60
ATOM   1367  SD  MET A 235      26.597  36.751  25.819  1.00 20.56
ATOM   1368  CE  MET A 235      25.105  36.803  24.857  1.00 21.69
ATOM   1369  N   ILE A 236      29.629  40.248  22.801  1.00 19.70
ATOM   1370  CA  ILE A 236      29.271  41.669  22.674  1.00 19.40
ATOM   1371  C   ILE A 236      27.764  41.758  22.522  1.00 20.06
ATOM   1372  O   ILE A 236      27.175  41.365  21.467  1.00 16.87
ATOM   1373  CB  ILE A 236      29.985  42.341  21.470  1.00 21.41
ATOM   1374  CG1 ILE A 236      31.452  42.625  21.821  1.00 22.57
ATOM   1375  CG2 ILE A 236      29.329  43.672  21.149  1.00 21.72
ATOM   1376  CD1 ILE A 236      32.243  41.426  22.228  1.00 25.65
ATOM   1377  N   ILE A 237      27.122  42.246  23.575  1.00 20.16
ATOM   1378  CA  ILE A 237      25.663  42.382  23.599  1.00 21.01
ATOM   1379  C   ILE A 237      25.215  43.710  22.996  1.00 22.16
ATOM   1380  O   ILE A 237      25.620  44.812  23.472  1.00 22.96
ATOM   1381  CB  ILE A 237      25.153  42.241  25.050  1.00 21.36
ATOM   1382  CG1 ILE A 237      25.346  40.791  25.498  1.00 22.29
ATOM   1383  CG2 ILE A 237      23.694  42.660  25.156  1.00 20.45
ATOM   1384  CD1 ILE A 237      25.002  40.529  26.939  1.00 24.84
ATOM   1385  N   GLY A 238      24.404  43.626  21.946  1.00 23.30
ATOM   1386  CA  GLY A 238      23.903  44.820  21.288  1.00 25.11
ATOM   1387  C   GLY A 238      24.821  45.437  20.244  1.00 26.35
ATOM   1388  O   GLY A 238      24.644  46.640  19.874  1.00 27.08
ATOM   1389  N   GLY A 239      25.792  44.681  19.743  1.00 25.50
ATOM   1390  CA  GLY A 239      26.679  45.251  18.747  1.00 24.81
ATOM   1391  C   GLY A 239      27.807  44.371  18.242  1.00 26.38
ATOM   1392  O   GLY A 239      27.942  43.167  18.632  1.00 23.61
ATOM   1393  N   ILE A 240      28.632  44.960  17.383  1.00 26.33
ATOM   1394  CA  ILE A 240      29.780  44.273  16.758  1.00 25.87
ATOM   1395  C   ILE A 240      31.067  45.033  17.055  1.00 26.95
ATOM   1396  O   ILE A 240      31.121  46.287  16.882  1.00 28.86
ATOM   1397  CB  ILE A 240      29.607  44.226  15.226  1.00 25.88
ATOM   1398  CG1 ILE A 240      28.298  43.519  14.871  1.00 25.12
ATOM   1399  CG2 ILE A 240      30.806  43.541  14.581  1.00 26.56
ATOM   1400  CD1 ILE A 240      27.939  43.599  13.396  1.00 24.59
ATOM   1401  N   ASP A 241      32.100  44.323  17.498  1.00 25.24
ATOM   1402  CA  ASP A 241      33.395  44.973  17.781  1.00 25.13
ATOM   1403  C   ASP A 241      34.383  44.548  16.698  1.00 26.31
ATOM   1404  O   ASP A 241      34.676  43.326  16.536  1.00 26.89
ATOM   1405  CB  ASP A 241      33.922  44.561  19.153  1.00 24.85
ATOM   1406  CG  ASP A 241      35.171  45.325  19.541  1.00 24.81
ATOM   1407  OD1 ASP A 241      35.144  46.032  20.567  1.00 27.86
ATOM   1408  OD2 ASP A 241      36.180  45.226  18.817  1.00 25.69
ATOM   1409  N   HIS A 242      34.913  45.517  15.960  1.00 26.86
ATOM   1410  CA  HIS A 242      35.853  45.222  14.852  1.00 27.45
ATOM   1411  C   HIS A 242      37.197  44.613  15.221  1.00 25.41
ATOM   1412  O   HIS A 242      37.871  43.998  14.347  1.00 23.94
ATOM   1413  CB  HIS A 242      36.085  46.481  14.013  1.00 32.38
ATOM   1414  CG  HIS A 242      34.858  46.957  13.304  1.00 37.46
ATOM   1415  ND1 HIS A 242      33.822  47.591  13.956  1.00 39.65
ATOM   1416  CD2 HIS A 242      34.472  46.837  12.011  1.00 39.29
ATOM   1417  CE1 HIS A 242      32.850  47.840  13.096  1.00 40.56
ATOM   1418  NE2 HIS A 242      33.219  47.392  11.909  1.00 40.36
ATOM   1419  N   SER A 243      37.615  44.751  16.471  1.00 22.23
ATOM   1420  CA  SER A 243      38.915  44.184  16.877  1.00 22.06
ATOM   1421  C   SER A 243      38.843  42.667  17.011  1.00 20.51
ATOM   1422  O   SER A 243      39.897  41.986  17.130  1.00 23.23
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ATOM   1423  CB  SER A 243      39.368  44.785  18.211  1.00 22.47
ATOM   1424  OG  SER A 243      38.515  44.386  19.274  1.00 23.32
ATOM   1425  N   LEU A 244      37.635  42.115  16.979  1.00 20.52
ATOM   1426  CA  LEU A 244      37.454  40.649  17.145  1.00 18.32
ATOM   1427  C   LEU A 244      37.535  39.844  15.860  1.00 18.66
ATOM   1428  O   LEU A 244      37.482  38.576  15.892  1.00 18.25
ATOM   1429  CB  LEU A 244      36.120  40.368  17.843  1.00 18.01
ATOM   1430  CG  LEU A 244      35.998  41.054  19.206  1.00 17.93
ATOM   1431  CD1 LEU A 244      34.689  40.666  19.885  1.00 17.04
ATOM   1432  CD2 LEU A 244      37.189  40.661  20.063  1.00 19.23
ATOM   1433  N   TYR A 245      37.666  40.522  14.729  1.00 18.73
ATOM   1434  CA  TYR A 245      37.756  39.795  13.459  1.00 19.72
ATOM   1435  C   TYR A 245      38.536  40.545  12.398  1.00 20.55
ATOM   1436  O   TYR A 245      38.819  41.771  12.542  1.00 21.10
ATOM   1437  CB  TYR A 245      36.357  39.494  12.924  1.00 19.56
ATOM   1438  CG  TYR A 245      35.606  40.708  12.421  1.00 20.40
ATOM   1439  CD1 TYR A 245      34.977  41.586  13.302  1.00 20.11
ATOM   1440  CD2 TYR A 245      35.512  40.966  11.055  1.00 20.70
ATOM   1441  CE1 TYR A 245      34.265  42.689  12.834  1.00 21.90
ATOM   1442  CE2 TYR A 245      34.809  42.060  10.573  1.00 22.10
ATOM   1443  CZ  TYR A 245      34.184  42.919  11.466  1.00 23.05
ATOM   1444  OH  TYR A 245      33.476  43.993  10.979  1.00 22.53
ATOM   1445  N   THR A 246      38.902  39.829  11.340  1.00 20.48
ATOM   1446  CA  THR A 246      39.621  40.429  10.195  1.00 19.46
ATOM   1447  C   THR A 246      38.811  40.054   8.964  1.00 19.29
ATOM   1448  O   THR A 246      37.999  39.085   9.000  1.00 16.84
ATOM   1449  CB  THR A 246      41.049  39.865  10.031  1.00 19.69
ATOM   1450  OG1 THR A 246      40.997  38.434   9.953  1.00 20.05
ATOM   1451  CG2 THR A 246      41.929  40.294  11.194  1.00 19.01
ATOM   1452  N   GLY A 247      38.996  40.793   7.879  1.00 19.48
ATOM   1453  CA  GLY A 247      38.259  40.490   6.668  1.00 19.61
ATOM   1454  C   GLY A 247      36.812  40.927   6.747  1.00 20.26
ATOM   1455  O   GLY A 247      36.412  41.712   7.660  1.00 21.64
ATOM   1456  N   SER A 248      36.006  40.437   5.816  1.00 21.23
ATOM   1457  CA  SER A 248      34.580  40.806   5.765  1.00 23.54
ATOM   1458  C   SER A 248      33.649  39.836   6.484  1.00 23.00
ATOM   1459  O   SER A 248      33.978  38.625   6.684  1.00 21.96
ATOM   1460  CB  SER A 248      34.135  40.936   4.304  1.00 24.06
ATOM   1461  OG  SER A 248      34.814  41.999   3.656  1.00 28.27
ATOM   1462  N   LEU A 249      32.494  40.355   6.881  1.00 23.33
ATOM   1463  CA  LEU A 249      31.453  39.551   7.550  1.00 23.71
ATOM   1464  C   LEU A 249      30.478  39.103   6.468  1.00 23.26
ATOM   1465  O   LEU A 249      29.913  39.958   5.721  1.00 24.66
ATOM   1466  CB  LEU A 249      30.687  40.392   8.576  1.00 22.83
ATOM   1467  CG  LEU A 249      31.234  40.585   9.992  1.00 23.68
ATOM   1468  CD1 LEU A 249      30.483  41.728  10.659  1.00 23.07
ATOM   1469  CD2 LEU A 249      31.077  39.299  10.802  1.00 22.16
ATOM   1470  N   TRP A 250      30.285  37.797   6.335  1.00 21.28
ATOM   1471  CA  TRP A 250      29.328  37.282   5.348  1.00 18.03
ATOM   1472  C   TRP A 250      28.115  36.810   6.115  1.00 18.51
ATOM   1473  O   TRP A 250      28.242  36.079   7.153  1.00 18.65
ATOM   1474  CB  TRP A 250      29.925  36.128   4.550  1.00 19.15
ATOM   1475  CG  TRP A 250      30.759  36.597   3.411  1.00 19.10
ATOM   1476  CD1 TRP A 250      32.061  36.998   3.456  1.00 18.51
ATOM   1477  CD2 TRP A 250      30.328  36.777   2.058  1.00 18.74
ATOM   1478  NE1 TRP A 250      32.470  37.418   2.214  1.00 18.41
ATOM   1479  CE2 TRP A 250      31.425  37.294   1.336  1.00 18.71
ATOM   1480  CE3 TRP A 250      29.118  36.554   1.386  1.00 19.61
ATOM   1481  CZ2 TRP A 250      31.352  37.594  -0.029  1.00 18.57
ATOM   1482  CZ3 TRP A 250      29.043  36.853   0.026  1.00 20.92
ATOM   1483  CH2 TRP A 250      30.158  37.369  -0.666  1.00 17.98
ATOM   1484  N   TYR A 251      26.939  37.203   5.644  1.00 17.22
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ATOM   1485  CA  TYR A 251      25.699  36.825   6.328  1.00 16.85
ATOM   1486  C   TYR A 251      24.875  35.751   5.642  1.00 16.82
ATOM   1487  O   TYR A 251      24.668  35.782   4.397  1.00 17.05
ATOM   1488  CB  TYR A 251      24.814  38.059   6.536  1.00 17.46
ATOM   1489  CG  TYR A 251      25.389  39.070   7.493  1.00 17.27
ATOM   1490  CD1 TYR A 251      26.265  40.065   7.055  1.00 18.34
ATOM   1491  CD2 TYR A 251      25.076  39.018   8.852  1.00 16.39
ATOM   1492  CE1 TYR A 251      26.819  40.984   7.955  1.00 18.20
ATOM   1493  CE2 TYR A 251      25.622  39.925   9.753  1.00 17.81
ATOM   1494  CZ  TYR A 251      26.487  40.900   9.302  1.00 17.43
ATOM   1495  OH  TYR A 251      27.014  41.779  10.215  1.00 20.25
ATOM   1496  N   THR A 252      24.395  34.803   6.436  1.00 15.07
ATOM   1497  CA  THR A 252      23.525  33.725   5.933  1.00 14.48
ATOM   1498  C   THR A 252      22.204  33.996   6.646  1.00 16.15
ATOM   1499  O   THR A 252      22.193  34.429   7.845  1.00 16.66
ATOM   1500  CB  THR A 252      24.056  32.325   6.330  1.00 14.69
ATOM   1501  OG1 THR A 252      23.273  31.316   5.684  1.00 13.97
ATOM   1502  CG2 THR A 252      23.974  32.118   7.839  1.00 14.05
ATOM   1503  N   PRO A 253      21.070  33.774   5.972  1.00 15.93
ATOM   1504  CA  PRO A 253      19.826  34.054   6.694  1.00 17.09
ATOM   1505  C   PRO A 253      19.418  33.029   7.741  1.00 18.67
ATOM   1506  O   PRO A 253      19.782  31.813   7.653  1.00 17.11
ATOM   1507  CB  PRO A 253      18.789  34.161   5.572  1.00 17.20
ATOM   1508  CG  PRO A 253      19.304  33.207   4.545  1.00 17.18
ATOM   1509  CD  PRO A 253      20.809  33.468   4.553  1.00 17.14
ATOM   1510  N   ILE A 254      18.692  33.501   8.750  1.00 18.82
ATOM   1511  CA  ILE A 254      18.165  32.604   9.792  1.00 20.14
ATOM   1512  C   ILE A 254      16.885  32.091   9.137  1.00 21.33
ATOM   1513  O   ILE A 254      15.911  32.875   8.914  1.00 21.52
ATOM   1514  CB  ILE A 254      17.827  33.368  11.091  1.00 20.62
ATOM   1515  CG1 ILE A 254      19.124  33.752  11.806  1.00 20.82
ATOM   1516  CG2 ILE A 254      16.935  32.509  11.994  1.00 19.41
ATOM   1517  CD1 ILE A 254      18.920  34.458  13.127  1.00 22.19
ATOM   1518  N   ARG A 255      16.868  30.810   8.795  1.00 22.06
ATOM   1519  CA  ARG A 255      15.702  30.211   8.115  1.00 23.47
ATOM   1520  C   ARG A 255      14.398  30.343   8.880  1.00 24.68
ATOM   1521  O   ARG A 255      13.334  30.719   8.299  1.00 25.49
ATOM   1522  CB  ARG A 255      15.951  28.735   7.852  1.00 22.62
ATOM   1523  CG  ARG A 255      14.843  28.093   7.053  1.00 22.10
ATOM   1524  CD  ARG A 255      14.985  26.598   7.069  1.00 22.76
ATOM   1525  NE  ARG A 255      14.031  25.958   6.176  1.00 22.51
ATOM   1526  CZ  ARG A 255      13.692  24.679   6.256  1.00 22.37
ATOM   1527  NH1 ARG A 255      14.232  23.914   7.195  1.00 20.91
ATOM   1528  NH2 ARG A 255      12.819  24.166   5.396  1.00 23.78
ATOM   1529  N   ARG A 256      14.451  30.023  10.165  1.00 24.98
ATOM   1530  CA  ARG A 256      13.264  30.085  11.029  1.00 25.56
ATOM   1531  C   ARG A 256      13.723  30.441  12.438  1.00 24.84
ATOM   1532  O   ARG A 256      14.829  30.013  12.893  1.00 22.14
ATOM   1533  CB  ARG A 256      12.561  28.729  11.009  1.00 27.37
ATOM   1534  CG  ARG A 256      11.350  28.599  11.914  1.00 29.24
ATOM   1535  CD  ARG A 256      10.878  27.150  11.899  1.00 29.60
ATOM   1536  NE  ARG A 256      10.180  26.788  13.126  1.00 31.29
ATOM   1537  CZ  ARG A 256      10.043  25.543  13.563  1.00 31.25
ATOM   1538  NH1 ARG A 256      10.559  24.535  12.870  1.00 31.19
ATOM   1539  NH2 ARG A 256       9.398  25.307  14.698  1.00 32.97
ATOM   1540  N   GLU A 257      12.914  31.219  13.141  1.00 24.01
ATOM   1541  CA  GLU A 257      13.270  31.650  14.500  1.00 23.46
ATOM   1542  C   GLU A 257      12.829  30.739  15.636  1.00 23.02
ATOM   1543  O   GLU A 257      11.749  30.947  16.264  1.00 26.15
ATOM   1544  CB  GLU A 257      12.739  33.055  14.748  1.00 23.25
ATOM   1545  CG  GLU A 257      13.439  34.123  13.930  1.00 26.24
ATOM   1546  CD  GLU A 257      12.572  35.353  13.746  1.00 27.27
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ATOM   1547  OE1 GLU A 257      13.124  36.470  13.673  1.00 27.35
ATOM   1548  OE2 GLU A 257      11.334  35.197  13.665  1.00 30.46
ATOM   1549  N   TRP A 258      13.632  29.719  15.898  1.00 19.64
ATOM   1550  CA  TRP A 258      13.390  28.798  17.016  1.00 19.75
ATOM   1551  C   TRP A 258      14.812  28.548  17.495  1.00 19.46
ATOM   1552  O   TRP A 258      15.267  29.190  18.500  1.00 20.47
ATOM   1553  CB  TRP A 258      12.632  27.537  16.561  1.00 18.27
ATOM   1554  CG  TRP A 258      13.203  26.710  15.455  1.00 17.96
ATOM   1555  CD1 TRP A 258      13.898  27.143  14.364  1.00 18.43
ATOM   1556  CD2 TRP A 258      13.051  25.293  15.298  1.00 17.87
ATOM   1557  NE1 TRP A 258      14.187  26.082  13.537  1.00 18.62
ATOM   1558  CE2 TRP A 258      13.678  24.935  14.088  1.00 17.86
ATOM   1559  CE3 TRP A 258      12.441  24.291  16.067  1.00 17.50
ATOM   1560  CZ2 TRP A 258      13.717  23.614  13.624  1.00 19.19
ATOM   1561  CZ3 TRP A 258      12.477  22.976  15.608  1.00 19.16
ATOM   1562  CH2 TRP A 258      13.113  22.650  14.396  1.00 18.86
ATOM   1563  N   TYR A 259      15.538  27.670  16.814  1.00 18.33
ATOM   1564  CA  TYR A 259      16.965  27.458  17.126  1.00 15.42
ATOM   1565  C   TYR A 259      17.550  28.474  16.157  1.00 16.46
ATOM   1566  O   TYR A 259      16.789  29.066  15.323  1.00 15.71
ATOM   1567  CB  TYR A 259      17.439  26.078  16.671  1.00 13.86
ATOM   1568  CG  TYR A 259      17.056  24.927  17.564  1.00 13.98
ATOM   1569  CD1 TYR A 259      17.876  24.539  18.627  1.00 13.32
ATOM   1570  CD2 TYR A 259      15.875  24.224  17.346  1.00 12.14
ATOM   1571  CE1 TYR A 259      17.520  23.467  19.450  1.00 15.06
ATOM   1572  CE2 TYR A 259      15.510  23.167  18.155  1.00 14.24
ATOM   1573  CZ  TYR A 259      16.329  22.789  19.200  1.00 14.26
ATOM   1574  OH  TYR A 259      15.940  21.719  19.955  1.00 12.92
ATOM   1575  N   TYR A 260      18.851  28.725  16.224  1.00 14.50
ATOM   1576  CA  TYR A 260      19.440  29.630  15.232  1.00 15.21
ATOM   1577  C   TYR A 260      19.716  28.718  14.037  1.00 15.90
ATOM   1578  O   TYR A 260      20.866  28.210  13.836  1.00 16.76
ATOM   1579  CB  TYR A 260      20.722  30.269  15.759  1.00 13.84
ATOM   1580  CG  TYR A 260      20.426  31.416  16.690  1.00 14.32
ATOM   1581  CD1 TYR A 260      20.534  31.270  18.078  1.00 13.41
ATOM   1582  CD2 TYR A 260      19.996  32.642  16.187  1.00 13.45
ATOM   1583  CE1 TYR A 260      20.224  32.320  18.933  1.00 13.15
ATOM   1584  CE2 TYR A 260      19.680  33.699  17.037  1.00 12.56
ATOM   1585  CZ  TYR A 260      19.801  33.530  18.404  1.00 13.22
ATOM   1586  OH  TYR A 260      19.531  34.582  19.239  1.00 12.88
ATOM   1587  N   GLU A 261      18.664  28.476  13.260  1.00 15.81
ATOM   1588  CA  GLU A 261      18.741  27.586  12.081  1.00 17.54
ATOM   1589  C   GLU A 261      19.191  28.266  10.791  1.00 17.31
ATOM   1590  O   GLU A 261      18.665  29.355  10.402  1.00 16.63
ATOM   1591  CB  GLU A 261      17.382  26.914  11.842  1.00 16.53
ATOM   1592  CG  GLU A 261      17.326  26.076  10.573  1.00 19.47
ATOM   1593  CD  GLU A 261      15.965  25.454  10.326  1.00 20.18
ATOM   1594  OE1 GLU A 261      14.956  26.037  10.766  1.00 21.27
ATOM   1595  OE2 GLU A 261      15.902  24.390   9.673  1.00 20.94
ATOM   1596  N   VAL A 262      20.153  27.640  10.122  1.00 16.45
ATOM   1597  CA  VAL A 262      20.679  28.147   8.842  1.00 16.13
ATOM   1598  C   VAL A 262      20.620  27.006   7.831  1.00 17.33
ATOM   1599  O   VAL A 262      20.168  25.863   8.166  1.00 17.30
ATOM   1600  CB  VAL A 262      22.131  28.624   8.982  1.00 14.58
ATOM   1601  CG1 VAL A 262      22.218  29.690  10.064  1.00 14.84
ATOM   1602  CG2 VAL A 262      23.039  27.449   9.308  1.00 14.53
ATOM   1603  N   ILE A 263      21.064  27.271   6.608  1.00 17.34
ATOM   1604  CA  ILE A 263      21.044  26.245   5.554  1.00 16.67
ATOM   1605  C   ILE A 263      22.419  26.042   4.931  1.00 16.64
ATOM   1606  O   ILE A 263      23.054  27.016   4.418  1.00 17.50
ATOM   1607  CB  ILE A 263      20.031  26.619   4.445  1.00 18.45
ATOM   1608  CG1 ILE A 263      18.608  26.522   4.996  1.00 18.90
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ATOM   1609  CG2 ILE A 263      20.192  25.694   3.243  1.00 18.17
ATOM   1610  CD1 ILE A 263      17.541  26.974   4.023  1.00 23.31
ATOM   1611  N   ILE A 264      22.897  24.802   4.988  1.00 16.67
ATOM   1612  CA  ILE A 264      24.199  24.413   4.409  1.00 14.63
ATOM   1613  C   ILE A 264      23.882  23.836   3.031  1.00 16.44
ATOM   1614  O   ILE A 264      23.019  22.915   2.908  1.00 13.53
ATOM   1615  CB  ILE A 264      24.877  23.320   5.253  1.00 14.79
ATOM   1616  CG1 ILE A 264      25.174  23.855   6.657  1.00 12.53
ATOM   1617  CG2 ILE A 264      26.154  22.846   4.563  1.00 12.07
ATOM   1618  CD1 ILE A 264      25.685  22.799   7.615  1.00 12.69
ATOM   1619  N   VAL A 265      24.546  24.334   1.992  1.00 17.37
ATOM   1620  CA  VAL A 265      24.258  23.841   0.627  1.00 18.64
ATOM   1621  C   VAL A 265      25.368  23.004   0.006  1.00 19.95
ATOM   1622  O   VAL A 265      25.202  22.455  -1.127  1.00 19.29
ATOM   1623  CB  VAL A 265      23.956  25.011  -0.322  1.00 18.56
ATOM   1624  CG1 VAL A 265      22.874  25.901   0.287  1.00 16.70
ATOM   1625  CG2 VAL A 265      25.227  25.802  -0.590  1.00 17.47
ATOM   1626  N   ARG A 266      26.486  22.872   0.707  1.00 20.42
ATOM   1627  CA  ARG A 266      27.617  22.098   0.165  1.00 20.48
ATOM   1628  C   ARG A 266      28.752  22.044   1.162  1.00 19.59
ATOM   1629  O   ARG A 266      29.030  23.055   1.885  1.00 19.51
ATOM   1630  CB  ARG A 266      28.112  22.763  -1.129  1.00 22.33
ATOM   1631  CG  ARG A 266      29.417  22.218  -1.713  1.00 22.40
ATOM   1632  CD  ARG A 266      29.939  23.170  -2.789  1.00 24.49
ATOM   1633  NE  ARG A 266      31.244  22.785  -3.322  1.00 24.49
ATOM   1634  CZ  ARG A 266      31.444  22.266  -4.528  1.00 26.46
ATOM   1635  NH1 ARG A 266      30.426  22.061  -5.349  1.00 25.31
ATOM   1636  NH2 ARG A 266      32.672  21.956  -4.920  1.00 27.88
ATOM   1637  N   VAL A 267      29.404  20.891   1.246  1.00 18.31
ATOM   1638  CA  VAL A 267      30.561  20.766   2.136  1.00 18.32
ATOM   1639  C   VAL A 267      31.671  20.072   1.369  1.00 18.25
ATOM   1640  O   VAL A 267      31.409  19.192   0.489  1.00 19.14
ATOM   1641  CB  VAL A 267      30.248  19.974   3.456  1.00 18.72
ATOM   1642  CG1 VAL A 267      28.784  19.645   3.547  1.00 18.30
ATOM   1643  CG2 VAL A 267      31.112  18.728   3.554  1.00 17.65
ATOM   1644  N   GLU A 268      32.903  20.471   1.647  1.00 16.18
ATOM   1645  CA  GLU A 268      34.046  19.848   0.990  1.00 17.71
ATOM   1646  C   GLU A 268      35.169  19.546   1.970  1.00 16.08
ATOM   1647  O   GLU A 268      35.293  20.191   3.064  1.00 13.62
ATOM   1648  CB  GLU A 268      34.550  20.717  -0.177  1.00 18.50
ATOM   1649  CG  GLU A 268      34.430  22.207   0.030  1.00 22.46
ATOM   1650  CD  GLU A 268      34.888  23.016  -1.181  1.00 22.13
ATOM   1651  OE1 GLU A 268      34.216  22.970  -2.237  1.00 20.91
ATOM   1652  OE2 GLU A 268      35.927  23.703  -1.067  1.00 22.44
ATOM   1653  N   ILE A 269      35.948  18.531   1.623  1.00 13.57
ATOM   1654  CA  ILE A 269      37.103  18.112   2.418  1.00 13.89
ATOM   1655  C   ILE A 269      38.259  18.448   1.485  1.00 14.06
ATOM   1656  O   ILE A 269      38.396  17.832   0.386  1.00 14.03
ATOM   1657  CB  ILE A 269      37.051  16.596   2.703  1.00 14.48
ATOM   1658  CG1 ILE A 269      35.697  16.239   3.327  1.00 14.59
ATOM   1659  CG2 ILE A 269      38.180  16.193   3.645  1.00 12.12
ATOM   1660  CD1 ILE A 269      35.358  17.022   4.592  1.00 13.16
ATOM   1661  N   ASN A 270      39.067  19.431   1.872  1.00 14.16
ATOM   1662  CA  ASN A 270      40.205  19.886   1.038  1.00 13.20
ATOM   1663  C   ASN A 270      39.774  20.177  -0.399  1.00 13.24
ATOM   1664  O   ASN A 270      40.427  19.714  -1.385  1.00 13.72
ATOM   1665  CB  ASN A 270      41.336  18.852   1.047  1.00 11.19
ATOM   1666  CG  ASN A 270      42.424  19.186   2.054  1.00 13.23
ATOM   1667  OD1 ASN A 270      42.339  20.224   2.790  1.00 13.62
ATOM   1668  ND2 ASN A 270      43.454  18.348   2.117  1.00 11.67
ATOM   1669  N   GLY A 271      38.691  20.932  -0.540  1.00 13.07
ATOM   1670  CA  GLY A 271      38.210  21.302  -1.858  1.00 13.58
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ATOM   1671  C   GLY A 271      37.393  20.241  -2.564  1.00 14.87
ATOM   1672  O   GLY A 271      36.704  20.545  -3.581  1.00 13.70
ATOM   1673  N   GLN A 272      37.447  19.005  -2.076  1.00 14.64
ATOM   1674  CA  GLN A 272      36.674  17.914  -2.705  1.00 14.45
ATOM   1675  C   GLN A 272      35.261  17.870  -2.140  1.00 15.83
ATOM   1676  O   GLN A 272      35.050  17.717  -0.902  1.00 15.81
ATOM   1677  CB  GLN A 272      37.357  16.561  -2.486  1.00 14.85
ATOM   1678  CG  GLN A 272      36.692  15.421  -3.250  1.00 14.45
ATOM   1679  CD  GLN A 272      37.499  14.135  -3.211  1.00 16.34
ATOM   1680  OE1 GLN A 272      37.097  13.134  -2.535  1.00 20.05
ATOM   1681  NE2 GLN A 272      38.633  14.121  -3.909  1.00 13.09
ATOM   1682  N   ASP A 273      34.291  17.995  -3.035  1.00 16.17
ATOM   1683  CA  ASP A 273      32.857  17.987  -2.686  1.00 17.89
ATOM   1684  C   ASP A 273      32.388  16.612  -2.201  1.00 16.92
ATOM   1685  O   ASP A 273      32.713  15.566  -2.831  1.00 16.53
ATOM   1686  CB  ASP A 273      32.060  18.395  -3.930  1.00 20.38
ATOM   1687  CG  ASP A 273      30.576  18.526  -3.665  1.00 20.89
ATOM   1688  OD1 ASP A 273      29.827  18.788  -4.630  1.00 21.98
ATOM   1689  OD2 ASP A 273      30.155  18.378  -2.503  1.00 22.40
ATOM   1690  N   LEU A 274      31.639  16.576  -1.101  1.00 17.95
ATOM   1691  CA  LEU A 274      31.117  15.285  -0.587  1.00 19.37
ATOM   1692  C   LEU A 274      30.092  14.805  -1.598  1.00 21.18
ATOM   1693  O   LEU A 274      29.702  13.603  -1.623  1.00 20.08
ATOM   1694  CB  LEU A 274      30.451  15.455   0.783  1.00 18.46
ATOM   1695  CG  LEU A 274      31.356  15.595   2.011  1.00 19.89
ATOM   1696  CD1 LEU A 274      30.489  15.558   3.267  1.00 17.23
ATOM   1697  CD2 LEU A 274      32.392  14.463   2.050  1.00 17.76
ATOM   1698  N   LYS A 275      29.646  15.736  -2.431  1.00 24.29
ATOM   1699  CA  LYS A 275      28.676  15.452  -3.501  1.00 29.08
ATOM   1700  C   LYS A 275      27.439  14.715  -3.000  1.00 28.92
ATOM   1701  O   LYS A 275      27.119  13.586  -3.464  1.00 30.50
ATOM   1702  CB  LYS A 275      29.360  14.642  -4.608  1.00 30.50
ATOM   1703  CG  LYS A 275      28.720  14.818  -5.970  1.00 33.82
ATOM   1704  CD  LYS A 275      29.476  14.059  -7.042  1.00 36.63
ATOM   1705  CE  LYS A 275      28.848  14.297  -8.408  1.00 38.29
ATOM   1706  NZ  LYS A 275      28.742  15.759  -8.702  1.00 39.43
ATOM   1707  N   MET A 276      26.734  15.329  -2.063  1.00 30.55
ATOM   1708  CA  MET A 276      25.519  14.722  -1.505  1.00 30.03
ATOM   1709  C   MET A 276      24.319  15.592  -1.815  1.00 30.11
ATOM   1710  O   MET A 276      24.465  16.818  -2.117  1.00 28.94
ATOM   1711  CB  MET A 276      25.641  14.576   0.011  1.00 30.29
ATOM   1712  CG  MET A 276      26.706  13.605   0.469  1.00 30.69
ATOM   1713  SD  MET A 276      26.687  13.418   2.261  1.00 32.94
ATOM   1714  CE  MET A 276      25.174  12.457   2.477  1.00 31.04
ATOM   1715  N   ASP A 277      23.136  14.994  -1.756  1.00 31.37
ATOM   1716  CA  ASP A 277      21.906  15.750  -1.994  1.00 33.34
ATOM   1717  C   ASP A 277      21.903  16.864  -0.955  1.00 33.96
ATOM   1718  O   ASP A 277      22.070  16.608   0.278  1.00 30.80
ATOM   1719  CB  ASP A 277      20.682  14.851  -1.818  1.00 36.24
ATOM   1720  CG  ASP A 277      19.377  15.595  -2.029  1.00 38.93
ATOM   1721  OD1 ASP A 277      18.332  14.925  -2.168  1.00 42.69
ATOM   1722  OD2 ASP A 277      19.386  16.844  -2.049  1.00 39.38
ATOM   1723  N   CYS A 278      21.732  18.089  -1.432  1.00 34.50
ATOM   1724  CA  CYS A 278      21.725  19.294  -0.581  1.00 37.44
ATOM   1725  C   CYS A 278      20.988  19.126   0.749  1.00 35.96
ATOM   1726  O   CYS A 278      21.503  19.540   1.834  1.00 34.38
ATOM   1727  CB  CYS A 278      21.108  20.460  -1.362  1.00 39.86
ATOM   1728  SG  CYS A 278      21.760  22.075  -0.852  1.00 50.09
ATOM   1729  N   LYS A 279      19.802  18.529   0.705  1.00 33.76
ATOM   1730  CA  LYS A 279      19.003  18.359   1.931  1.00 32.65
ATOM   1731  C   LYS A 279      19.584  17.430   2.996  1.00 30.06
ATOM   1732  O   LYS A 279      19.173  17.501   4.189  1.00 27.89
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ATOM   1733  CB  LYS A 279      17.574  17.939   1.567  1.00 34.74
ATOM   1734  CG  LYS A 279      17.459  16.765   0.612  1.00 39.08
ATOM   1735  CD  LYS A 279      17.576  15.429   1.326  1.00 41.32
ATOM   1736  CE  LYS A 279      17.185  14.289   0.393  1.00 42.86
ATOM   1737  NZ  LYS A 279      17.118  12.978   1.099  1.00 45.07
ATOM   1738  N   GLU A 280      20.525  16.570   2.621  1.00 27.06
ATOM   1739  CA  GLU A 280      21.141  15.659   3.612  1.00 26.22
ATOM   1740  C   GLU A 280      21.900  16.458   4.673  1.00 25.34
ATOM   1741  O   GLU A 280      21.920  16.074   5.886  1.00 23.01
ATOM   1742  CB  GLU A 280      22.109  14.693   2.928  1.00 27.98
ATOM   1743  CG  GLU A 280      21.459  13.725   1.946  1.00 31.24
ATOM   1744  CD  GLU A 280      20.486  12.765   2.610  1.00 32.55
ATOM   1745  OE1 GLU A 280      20.447  12.704   3.857  1.00 33.21
ATOM   1746  OE2 GLU A 280      19.763  12.058   1.878  1.00 34.72
ATOM   1747  N   TYR A 281      22.515  17.562   4.255  1.00 23.32
ATOM   1748  CA  TYR A 281      23.295  18.420   5.176  1.00 22.69
ATOM   1749  C   TYR A 281      22.415  19.082   6.219  1.00 23.40
ATOM   1750  O   TYR A 281      22.904  19.470   7.327  1.00 23.11
ATOM   1751  CB  TYR A 281      24.035  19.515   4.400  1.00 20.26
ATOM   1752  CG  TYR A 281      24.958  18.993   3.328  1.00 19.39
ATOM   1753  CD1 TYR A 281      25.858  17.961   3.601  1.00 17.78
ATOM   1754  CD2 TYR A 281      24.943  19.534   2.042  1.00 18.55
ATOM   1755  CE1 TYR A 281      26.719  17.478   2.623  1.00 17.05
ATOM   1756  CE2 TYR A 281      25.808  19.058   1.051  1.00 18.53
ATOM   1757  CZ  TYR A 281      26.692  18.028   1.355  1.00 17.87
ATOM   1758  OH  TYR A 281      27.558  17.533   0.407  1.00 18.13
ATOM   1759  N   ASN A 282      21.136  19.232   5.899  1.00 22.82
ATOM   1760  CA  ASN A 282      20.194  19.881   6.820  1.00 23.17
ATOM   1761  C   ASN A 282      19.089  18.922   7.238  1.00 23.84
ATOM   1762  O   ASN A 282      17.987  19.366   7.685  1.00 21.83
ATOM   1763  CB  ASN A 282      19.598  21.111   6.137  1.00 22.42
ATOM   1764  CG  ASN A 282      20.665  22.018   5.549  1.00 23.90
ATOM   1765  OD1 ASN A 282      21.426  22.693   6.298  1.00 23.87
ATOM   1766  ND2 ASN A 282      20.760  22.044   4.224  1.00 23.36
ATOM   1767  N   TYR A 283      19.343  17.623   7.102  1.00 25.74
ATOM   1768  CA  TYR A 283      18.322  16.633   7.472  1.00 28.01
ATOM   1769  C   TYR A 283      17.905  16.843   8.912  1.00 29.29
ATOM   1770  O   TYR A 283      18.686  16.572   9.881  1.00 27.50
ATOM   1771  CB  TYR A 283      18.810  15.200   7.280  1.00 29.52
ATOM   1772  CG  TYR A 283      17.783  14.200   7.756  1.00 31.64
ATOM   1773  CD1 TYR A 283      16.428  14.374   7.460  1.00 32.38
ATOM   1774  CD2 TYR A 283      18.153  13.098   8.523  1.00 33.44
ATOM   1775  CE1 TYR A 283      15.468  13.479   7.919  1.00 33.96
ATOM   1776  CE2 TYR A 283      17.201  12.194   8.987  1.00 35.48
ATOM   1777  CZ  TYR A 283      15.860  12.392   8.683  1.00 35.35
ATOM   1778  OH  TYR A 283      14.918  11.504   9.149  1.00 36.54
ATOM   1779  N   ASP A 284      16.665  17.299   9.043  1.00 30.23
ATOM   1780  CA  ASP A 284      16.026  17.638  10.312  1.00 28.41
ATOM   1781  C   ASP A 284      16.273  19.129  10.409  1.00 27.12
ATOM   1782  O   ASP A 284      15.309  19.953  10.305  1.00 25.19
ATOM   1783  CB  ASP A 284      16.684  16.928  11.494  1.00 33.07
ATOM   1784  CG  ASP A 284      16.035  17.283  12.813  1.00 33.49
ATOM   1785  OD1 ASP A 284      16.520  16.815  13.860  1.00 37.38
ATOM   1786  OD2 ASP A 284      15.035  18.031  12.802  1.00 35.95
ATOM   1787  N   LYS A 285      17.542  19.499  10.563  1.00 22.62
ATOM   1788  CA  LYS A 285      17.914  20.927  10.678  1.00 20.42
ATOM   1789  C   LYS A 285      19.420  21.145  10.812  1.00 19.89
ATOM   1790  O   LYS A 285      20.209  20.174  11.037  1.00 19.63
ATOM   1791  CB  LYS A 285      17.230  21.540  11.903  1.00 18.63
ATOM   1792  CG  LYS A 285      17.753  20.987  13.232  1.00 16.63
ATOM   1793  CD  LYS A 285      16.966  21.538  14.421  1.00 14.93
ATOM   1794  CE  LYS A 285      17.551  21.088  15.754  1.00 15.57
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ATOM	1795	NZ	LYS	A	285	17.482	19.606	15.974	1.00	13.50
ATOM	1796	N	SER	A	286	19.827	22.402	10.678	1.00	17.19
ATOM	1797	CA	SER	A	286	21.241	22.808	10.827	1.00	16.52
ATOM	1798	C	SER	A	286	21.228	24.034	11.727	1.00	15.74
ATOM	1799	O	SER	A	286	20.592	25.080	11.377	1.00	14.46
ATOM	1800	CB	SER	A	286	21.862	23.179	9.475	1.00	16.90
ATOM	1801	OG	SER	A	286	22.064	22.036	8.671	1.00	16.60
ATOM	1802	N	ILE	A	287	21.900	23.946	12.870	1.00	13.25
ATOM	1803	CA	ILE	A	287	21.933	25.079	13.805	1.00	13.97
ATOM	1804	C	ILE	A	287	23.342	25.511	14.206	1.00	15.14
ATOM	1805	O	ILE	A	287	24.346	24.750	14.024	1.00	14.63
ATOM	1806	CB	ILE	A	287	21.145	24.757	15.102	1.00	13.55
ATOM	1807	CG1	ILE	A	287	21.898	23.717	15.929	1.00	12.52
ATOM	1808	CG2	ILE	A	287	19.758	24.214	14.754	1.00	12.10
ATOM	1809	CD1	ILE	A	287	21.274	23.455	17.283	1.00	14.43
ATOM	1810	N	VAL	A	288	23.431	26.728	14.732	1.00	14.78
ATOM	1811	CA	VAL	A	288	24.701	27.292	15.223	1.00	15.54
ATOM	1812	C	VAL	A	288	24.510	27.262	16.733	1.00	16.05
ATOM	1813	O	VAL	A	288	23.571	27.930	17.278	1.00	15.61
ATOM	1814	CB	VAL	A	288	24.896	28.751	14.767	1.00	15.19
ATOM	1815	CG1	VAL	A	288	26.248	29.259	15.239	1.00	14.78
ATOM	1816	CG2	VAL	A	288	24.791	28.842	13.246	1.00	15.19
ATOM	1817	N	ASP	A	289	25.355	26.512	17.430	1.00	15.91
ATOM	1818	CA	ASP	A	289	25.194	26.373	18.891	1.00	14.81
ATOM	1819	C	ASP	A	289	26.467	26.444	19.724	1.00	15.27
ATOM	1820	O	ASP	A	289	27.322	25.504	19.700	1.00	15.75
ATOM	1821	CB	ASP	A	289	24.467	25.060	19.168	1.00	12.65
ATOM	1822	CG	ASP	A	289	24.264	24.806	20.634	1.00	13.29
ATOM	1823	OD1	ASP	A	289	24.372	25.768	21.426	1.00	11.88
ATOM	1824	OD2	ASP	A	289	23.981	23.639	20.988	1.00	10.63
ATOM	1825	N	SER	A	290	26.604	27.529	20.479	1.00	15.19
ATOM	1826	CA	SER	A	290	27.782	27.730	21.346	1.00	14.55
ATOM	1827	C	SER	A	290	27.770	26.748	22.510	1.00	15.43
ATOM	1828	O	SER	A	290	28.823	26.539	23.186	1.00	13.77
ATOM	1829	CB	SER	A	290	27.795	29.165	21.888	1.00	15.33
ATOM	1830	OG	SER	A	290	26.614	29.442	22.620	1.00	12.79
ATOM	1831	N	GLY	A	291	26.612	26.137	22.759	1.00	14.34
ATOM	1832	CA	GLY	A	291	26.486	25.192	23.856	1.00	14.93
ATOM	1833	C	GLY	A	291	26.779	23.751	23.479	1.00	16.64
ATOM	1834	O	GLY	A	291	26.502	22.792	24.277	1.00	14.49
ATOM	1835	N	THR	A	292	27.305	23.556	22.277	1.00	16.47
ATOM	1836	CA	THR	A	292	27.674	22.202	21.812	1.00	15.30
ATOM	1837	C	THR	A	292	29.159	22.215	21.482	1.00	14.67
ATOM	1838	O	THR	A	292	29.653	23.102	20.725	1.00	13.26
ATOM	1839	CB	THR	A	292	26.889	21.784	20.550	1.00	15.29
ATOM	1840	OG1	THR	A	292	25.522	21.521	20.895	1.00	13.88
ATOM	1841	CG2	THR	A	292	27.514	20.527	19.932	1.00	13.59
ATOM	1842	N	THR	A	293	29.887	21.253	22.027	1.00	14.43
ATOM	1843	CA	THR	A	293	31.343	21.162	21.801	1.00	12.76
ATOM	1844	C	THR	A	293	31.749	20.906	20.348	1.00	14.47
ATOM	1845	O	THR	A	293	32.478	21.735	19.712	1.00	14.61
ATOM	1846	CB	THR	A	293	31.949	20.035	22.650	1.00	12.36
ATOM	1847	OG1	THR	A	293	31.726	20.304	24.041	1.00	10.79
ATOM	1848	CG2	THR	A	293	33.437	19.916	22.382	1.00	9.56
ATOM	1849	N	ASN	A	294	31.286	19.783	19.810	1.00	13.53
ATOM	1850	CA	ASN	A	294	31.648	19.349	18.440	1.00	15.26
ATOM	1851	C	ASN	A	294	30.871	19.917	17.276	1.00	15.45
ATOM	1852	O	ASN	A	294	29.851	20.662	17.431	1.00	13.68
ATOM	1853	CB	ASN	A	294	31.494	17.832	18.307	1.00	14.81
ATOM	1854	CG	ASN	A	294	32.351	17.051	19.270	1.00	14.13
ATOM	1855	OD1	ASN	A	294	32.264	15.791	19.304	1.00	19.85
ATOM	1856	ND2	ASN	A	294	33.174	17.734	20.051	1.00	13.25

ATOM	1857	N	LEU	A	295	31.365	19.556	16.096	1.00	15.21
ATOM	1858	CA	LEU	A	295	30.689	19.866	14.835	1.00	15.29
ATOM	1859	C	LEU	A	295	29.924	18.548	14.719	1.00	16.43
ATOM	1860	O	LEU	A	295	30.556	17.452	14.575	1.00	16.34
ATOM	1861	CB	LEU	A	295	31.674	19.963	13.671	1.00	13.54
ATOM	1862	CG	LEU	A	295	31.017	19.837	12.287	1.00	14.74
ATOM	1863	CD1	LEU	A	295	29.991	20.947	12.109	1.00	14.37
ATOM	1864	CD2	LEU	A	295	32.073	19.903	11.179	1.00	13.91
ATOM	1865	N	ARG	A	296	28.606	18.591	14.831	1.00	16.08
ATOM	1866	CA	ARG	A	296	27.827	17.349	14.719	1.00	17.47
ATOM	1867	C	ARG	A	296	27.180	17.300	13.343	1.00	17.04
ATOM	1868	O	ARG	A	296	26.655	18.339	12.840	1.00	15.28
ATOM	1869	CB	ARG	A	296	26.785	17.290	15.834	1.00	18.37
ATOM	1870	CG	ARG	A	296	27.421	17.444	17.208	1.00	19.73
ATOM	1871	CD	ARG	A	296	26.425	17.262	18.324	1.00	22.63
ATOM	1872	NE	ARG	A	296	26.292	15.867	18.722	1.00	25.23
ATOM	1873	CZ	ARG	A	296	25.135	15.223	18.776	1.00	26.52
ATOM	1874	NH1	ARG	A	296	24.011	15.851	18.446	1.00	27.11
ATOM	1875	NH2	ARG	A	296	25.100	13.961	19.179	1.00	27.00
ATOM	1876	N	LEU	A	297	27.211	16.123	12.722	1.00	15.65
ATOM	1877	CA	LEU	A	297	26.660	15.945	11.356	1.00	15.33
ATOM	1878	C	LEU	A	297	25.657	14.800	11.246	1.00	17.46
ATOM	1879	O	LEU	A	297	25.795	13.743	11.938	1.00	16.37
ATOM	1880	CB	LEU	A	297	27.806	15.681	10.371	1.00	12.00
ATOM	1881	CG	LEU	A	297	28.925	16.729	10.277	1.00	11.84
ATOM	1882	CD1	LEU	A	297	30.136	16.148	9.561	1.00	8.16
ATOM	1883	CD2	LEU	A	297	28.410	17.962	9.559	1.00	8.99
ATOM	1884	N	PRO	A	298	24.636	14.960	10.386	1.00	19.11
ATOM	1885	CA	PRO	A	298	23.636	13.901	10.217	1.00	20.53
ATOM	1886	C	PRO	A	298	24.387	12.619	9.868	1.00	21.03
ATOM	1887	O	PRO	A	298	25.419	12.668	9.131	1.00	21.77
ATOM	1888	CB	PRO	A	298	22.788	14.411	9.054	1.00	19.18
ATOM	1889	CG	PRO	A	298	22.861	15.897	9.209	1.00	20.46
ATOM	1890	CD	PRO	A	298	24.335	16.111	9.517	1.00	19.69
ATOM	1891	N	LYS	A	299	23.911	11.487	10.376	1.00	22.77
ATOM	1892	CA	LYS	A	299	24.562	10.169	10.137	1.00	25.34
ATOM	1893	C	LYS	A	299	25.169	9.979	8.753	1.00	24.56
ATOM	1894	O	LYS	A	299	26.393	9.681	8.617	1.00	22.24
ATOM	1895	CB	LYS	A	299	23.566	9.034	10.387	1.00	29.05
ATOM	1896	CG	LYS	A	299	24.156	7.650	10.146	1.00	33.27
ATOM	1897	CD	LYS	A	299	23.144	6.547	10.408	1.00	37.10
ATOM	1898	CE	LYS	A	299	23.758	5.178	10.151	1.00	38.78
ATOM	1899	NZ	LYS	A	299	22.775	4.077	10.380	1.00	42.51
ATOM	1900	N	LYS	A	300	24.340	10.127	7.729	1.00	24.24
ATOM	1901	CA	LYS	A	300	24.774	9.955	6.333	1.00	25.41
ATOM	1902	C	LYS	A	300	25.901	10.916	5.952	1.00	24.12
ATOM	1903	O	LYS	A	300	26.889	10.515	5.262	1.00	23.67
ATOM	1904	CB	LYS	A	300	23.576	10.154	5.403	1.00	28.77
ATOM	1905	CG	LYS	A	300	23.788	9.660	3.990	1.00	33.37
ATOM	1906	CD	LYS	A	300	22.661	8.718	3.569	1.00	38.01
ATOM	1907	CE	LYS	A	300	21.298	9.393	3.652	1.00	40.18
ATOM	1908	NZ	LYS	A	300	20.191	8.455	3.291	1.00	42.69
ATOM	1909	N	VAL	A	301	25.784	12.172	6.368	1.00	20.46
ATOM	1910	CA	VAL	A	301	26.832	13.169	6.058	1.00	18.21
ATOM	1911	C	VAL	A	301	28.083	12.842	6.867	1.00	17.93
ATOM	1912	O	VAL	A	301	29.241	12.929	6.343	1.00	16.84
ATOM	1913	CB	VAL	A	301	26.358	14.601	6.391	1.00	17.29
ATOM	1914	CG1	VAL	A	301	27.468	15.605	6.105	1.00	15.43
ATOM	1915	CG2	VAL	A	301	25.118	14.935	5.565	1.00	16.34
ATOM	1916	N	PHE	A	302	27.887	12.448	8.122	1.00	17.43
ATOM	1917	CA	PHE	A	302	29.032	12.099	8.990	1.00	18.16
ATOM	1918	C	PHE	A	302	29.854	10.957	8.399	1.00	18.95

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ATOM   1919  O   PHE A 302      31.121  11.004   8.399  1.00 18.60
ATOM   1920  CB  PHE A 302      28.550  11.713  10.391  1.00 17.38
ATOM   1921  CG  PHE A 302      29.639  11.180  11.265  1.00 19.16
ATOM   1922  CD1 PHE A 302      29.866   9.810  11.362  1.00 17.81
ATOM   1923  CD2 PHE A 302      30.498  12.051  11.923  1.00 18.89
ATOM   1924  CE1 PHE A 302      30.934   9.320  12.096  1.00 19.63
ATOM   1925  CE2 PHE A 302      31.573  11.569  12.660  1.00 19.90
ATOM   1926  CZ  PHE A 302      31.793  10.201  12.747  1.00 19.13
ATOM   1927  N   GLU A 303      29.172   9.931   7.901  1.00 19.20
ATOM   1928  CA  GLU A 303      29.859   8.769   7.295  1.00 21.56
ATOM   1929  C   GLU A 303      30.679   9.189   6.083  1.00 19.19
ATOM   1930  O   GLU A 303      31.865   8.777   5.929  1.00 18.04
ATOM   1931  CB  GLU A 303      28.836   7.704   6.888  1.00 24.72
ATOM   1932  CG  GLU A 303      28.246   6.939   8.069  1.00 29.90
ATOM   1933  CD  GLU A 303      27.051   6.076   7.683  1.00 33.77
ATOM   1934  OE1 GLU A 303      26.585   5.294   8.541  1.00 36.31
ATOM   1935  OE2 GLU A 303      26.572   6.183   6.528  1.00 36.51
ATOM   1936  N   ALA A 304      30.088   9.998   5.216  1.00 17.86
ATOM   1937  CA  ALA A 304      30.805  10.472   4.007  1.00 18.11
ATOM   1938  C   ALA A 304      31.999  11.354   4.386  1.00 17.49
ATOM   1939  O   ALA A 304      33.102  11.242   3.777  1.00 17.76
ATOM   1940  CB  ALA A 304      29.849  11.244   3.102  1.00 17.14
ATOM   1941  N   ALA A 305      31.812  12.221   5.377  1.00 17.06
ATOM   1942  CA  ALA A 305      32.900  13.128   5.829  1.00 16.43
ATOM   1943  C   ALA A 305      34.092  12.387   6.440  1.00 16.39
ATOM   1944  O   ALA A 305      35.272  12.644   6.054  1.00 17.78
ATOM   1945  CB  ALA A 305      32.351  14.140   6.833  1.00 15.92
ATOM   1946  N   VAL A 306      33.842  11.476   7.375  1.00 15.50
ATOM   1947  CA  VAL A 306      34.971  10.756   8.004  1.00 17.31
ATOM   1948  C   VAL A 306      35.719   9.920   6.987  1.00 16.95
ATOM   1949  O   VAL A 306      36.983   9.829   7.029  1.00 16.21
ATOM   1950  CB  VAL A 306      34.514   9.845   9.162  1.00 17.93
ATOM   1951  CG1 VAL A 306      33.954  10.693  10.280  1.00 19.37
ATOM   1952  CG2 VAL A 306      33.477   8.851   8.669  1.00 19.63
ATOM   1953  N   LYS A 307      34.987   9.307   6.065  1.00 17.11
ATOM   1954  CA  LYS A 307      35.641   8.488   5.032  1.00 18.39
ATOM   1955  C   LYS A 307      36.654   9.350   4.279  1.00 17.59
ATOM   1956  O   LYS A 307      37.848   8.959   4.107  1.00 18.09
ATOM   1957  CB  LYS A 307      34.602   7.940   4.052  1.00 19.72
ATOM   1958  CG  LYS A 307      35.212   7.112   2.930  1.00 24.02
ATOM   1959  CD  LYS A 307      34.147   6.415   2.102  1.00 26.72
ATOM   1960  CE  LYS A 307      34.779   5.505   1.058  1.00 29.36
ATOM   1961  NZ  LYS A 307      33.745   4.869   0.193  1.00 31.68
ATOM   1962  N   SER A 308      36.205  10.520   3.842  1.00 16.75
ATOM   1963  CA  SER A 308      37.059  11.460   3.091  1.00 17.46
ATOM   1964  C   SER A 308      38.198  12.000   3.953  1.00 16.11
ATOM   1965  O   SER A 308      39.378  12.056   3.501  1.00 17.12
ATOM   1966  CB  SER A 308      36.208  12.620   2.560  1.00 17.51
ATOM   1967  OG  SER A 308      36.982  13.505   1.774  1.00 19.76
ATOM   1968  N   ILE A 309      37.886  12.400   5.180  1.00 16.07
ATOM   1969  CA  ILE A 309      38.926  12.927   6.083  1.00 14.41
ATOM   1970  C   ILE A 309      39.945  11.831   6.378  1.00 14.93
ATOM   1971  O   ILE A 309      41.171  12.112   6.505  1.00 14.90
ATOM   1972  CB  ILE A 309      38.310  13.439   7.401  1.00 13.88
ATOM   1973  CG1 ILE A 309      37.346  14.595   7.099  1.00 13.08
ATOM   1974  CG2 ILE A 309      39.404  13.887   8.350  1.00 11.40
ATOM   1975  CD1 ILE A 309      36.575  15.084   8.315  1.00 12.70
ATOM   1976  N   LYS A 310      39.475  10.592   6.485  1.00 15.62
ATOM   1977  CA  LYS A 310      40.375   9.437   6.752  1.00 17.74
ATOM   1978  C   LYS A 310      41.289   9.223   5.559  1.00 17.22
ATOM   1979  O   LYS A 310      42.532   9.061   5.715  1.00 16.87
ATOM   1980  CB  LYS A 310      39.577   8.149   6.976  1.00 18.35
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ATOM   1981  CG  LYS A 310      39.003   7.953   8.373  1.00 20.85
ATOM   1982  CD  LYS A 310      38.269   6.617   8.432  1.00 22.02
ATOM   1983  CE  LYS A 310      37.584   6.404   9.757  1.00 25.26
ATOM   1984  NZ  LYS A 310      36.808   5.129   9.752  1.00 26.15
ATOM   1985  N   ALA A 311      40.698   9.211   4.370  1.00 15.56
ATOM   1986  CA  ALA A 311      41.466   9.007   3.124  1.00 17.77
ATOM   1987  C   ALA A 311      42.549  10.071   2.990  1.00 17.36
ATOM   1988  O   ALA A 311      43.708   9.768   2.578  1.00 20.71
ATOM   1989  CB  ALA A 311      40.524   9.047   1.908  1.00 14.11
ATOM   1990  N   ALA A 312      42.210  11.309   3.330  1.00 16.63
ATOM   1991  CA  ALA A 312      43.184  12.418   3.235  1.00 15.73
ATOM   1992  C   ALA A 312      44.247  12.342   4.333  1.00 15.59
ATOM   1993  O   ALA A 312      45.348  12.958   4.207  1.00 13.09
ATOM   1994  CB  ALA A 312      42.449  13.758   3.301  1.00 13.50
ATOM   1995  N   SER A 313      43.950  11.593   5.393  1.00 17.05
ATOM   1996  CA  SER A 313      44.867  11.432   6.560  1.00 19.05
ATOM   1997  C   SER A 313      45.579  10.085   6.593  1.00 19.49
ATOM   1998  O   SER A 313      46.332   9.787   7.568  1.00 21.95
ATOM   1999  CB  SER A 313      44.075  11.555   7.865  1.00 17.23
ATOM   2000  OG  SER A 313      43.501  12.834   8.003  1.00 23.58
ATOM   2001  N   SER A 314      45.368   9.270   5.570  1.00 20.76
ATOM   2002  CA  SER A 314      45.952   7.909   5.513  1.00 22.73
ATOM   2003  C   SER A 314      47.436   7.725   5.838  1.00 21.90
ATOM   2004  O   SER A 314      47.825   6.639   6.359  1.00 20.76
ATOM   2005  CB  SER A 314      45.650   7.271   4.150  1.00 22.50
ATOM   2006  OG  SER A 314      46.207   8.032   3.093  1.00 27.94
ATOM   2007  N   THR A 315      48.285   8.714   5.570  1.00 20.90
ATOM   2008  CA  THR A 315      49.732   8.523   5.868  1.00 23.78
ATOM   2009  C   THR A 315      50.020   8.454   7.361  1.00 25.42
ATOM   2010  O   THR A 315      51.191   8.219   7.784  1.00 26.24
ATOM   2011  CB  THR A 315      50.616   9.634   5.257  1.00 23.59
ATOM   2012  OG1 THR A 315      50.256  10.901   5.818  1.00 22.73
ATOM   2013  CG2 THR A 315      50.456   9.668   3.745  1.00 22.59
ATOM   2014  N   GLU A 316      48.994   8.655   8.176  1.00 27.46
ATOM   2015  CA  GLU A 316      49.170   8.589   9.638  1.00 29.81
ATOM   2016  C   GLU A 316      48.258   7.503  10.201  1.00 30.55
ATOM   2017  O   GLU A 316      47.110   7.314   9.710  1.00 29.51
ATOM   2018  CB  GLU A 316      48.819   9.931  10.279  1.00 32.51
ATOM   2019  CG  GLU A 316      49.277  10.039  11.725  1.00 36.72
ATOM   2020  CD  GLU A 316      50.571  10.818  11.879  1.00 36.99
ATOM   2021  OE1 GLU A 316      51.456  10.728  11.003  1.00 37.39
ATOM   2022  OE2 GLU A 316      50.704  11.522  12.893  1.00 41.14
ATOM   2023  N   LYS A 317      48.736   6.775  11.205  1.00 32.69
ATOM   2024  CA  LYS A 317      47.928   5.702  11.828  1.00 35.09
ATOM   2025  C   LYS A 317      47.216   6.223  13.071  1.00 33.44
ATOM   2026  O   LYS A 317      47.804   7.005  13.883  1.00 34.13
ATOM   2027  CB  LYS A 317      48.809   4.505  12.202  1.00 38.52
ATOM   2028  CG  LYS A 317      49.980   4.844  13.106  1.00 43.41
ATOM   2029  CD  LYS A 317      50.665   3.588  13.638  1.00 46.99
ATOM   2030  CE  LYS A 317      51.165   2.686  12.514  1.00 48.65
ATOM   2031  NZ  LYS A 317      51.731   1.410  13.043  1.00 49.49
ATOM   2032  N   PHE A 318      45.965   5.818  13.245  1.00 31.00
ATOM   2033  CA  PHE A 318      45.188   6.272  14.408  1.00 30.33
ATOM   2034  C   PHE A 318      44.683   5.120  15.263  1.00 30.57
ATOM   2035  O   PHE A 318      44.171   4.088  14.732  1.00 29.80
ATOM   2036  CB  PHE A 318      44.014   7.135  13.944  1.00 28.83
ATOM   2037  CG  PHE A 318      44.436   8.367  13.197  1.00 28.31
ATOM   2038  CD1 PHE A 318      44.625   8.333  11.817  1.00 27.09
ATOM   2039  CD2 PHE A 318      44.686   9.554  13.879  1.00 27.59
ATOM   2040  CE1 PHE A 318      45.060   9.466  11.130  1.00 27.37
ATOM   2041  CE2 PHE A 318      45.122  10.691  13.200  1.00 26.98
ATOM   2042  CZ  PHE A 318      45.309  10.648  11.826  1.00 27.12
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ATOM   2043  N   PRO A 319      44.805   5.252  16.591  1.00 30.02
ATOM   2044  CA  PRO A 319      44.361   4.222  17.535  1.00 30.20
ATOM   2045  C   PRO A 319      42.864   3.977  17.460  1.00 29.88
ATOM   2046  O   PRO A 319      42.087   4.882  17.040  1.00 29.27
ATOM   2047  CB  PRO A 319      44.777   4.793  18.890  1.00 30.49
ATOM   2048  CG  PRO A 319      44.667   6.276  18.674  1.00 31.99
ATOM   2049  CD  PRO A 319      45.308   6.437  17.309  1.00 30.77
ATOM   2050  N   ASP A 320      42.449   2.779  17.860  1.00 30.08
ATOM   2051  CA  ASP A 320      41.018   2.389  17.867  1.00 29.79
ATOM   2052  C   ASP A 320      40.183   3.406  18.652  1.00 28.71
ATOM   2053  O   ASP A 320      40.560   3.804  19.804  1.00 27.90
ATOM   2054  CB  ASP A 320      40.855   1.009  18.520  1.00 31.81
ATOM   2055  CG  ASP A 320      41.545  -0.104  17.740  1.00 34.27
ATOM   2056  OD1 ASP A 320      41.787  -1.182  18.331  1.00 34.13
ATOM   2057  OD2 ASP A 320      41.833   0.092  16.538  1.00 35.41
ATOM   2058  N   GLY A 321      39.067   3.837  18.068  1.00 26.34
ATOM   2059  CA  GLY A 321      38.193   4.781  18.745  1.00 24.91
ATOM   2060  C   GLY A 321      38.439   6.259  18.490  1.00 23.96
ATOM   2061  O   GLY A 321      37.632   7.129  18.941  1.00 23.66
ATOM   2062  N   PHE A 322      39.519   6.591  17.793  1.00 22.07
ATOM   2063  CA  PHE A 322      39.810   8.011  17.507  1.00 20.41
ATOM   2064  C   PHE A 322      38.705   8.670  16.684  1.00 20.53
ATOM   2065  O   PHE A 322      38.157   9.743  17.078  1.00 20.75
ATOM   2066  CB  PHE A 322      41.126   8.157  16.747  1.00 19.07
ATOM   2067  CG  PHE A 322      41.405   9.567  16.306  1.00 19.05
ATOM   2068  CD1 PHE A 322      41.701  10.555  17.240  1.00 17.04
ATOM   2069  CD2 PHE A 322      41.326   9.918  14.960  1.00 17.20
ATOM   2070  CE1 PHE A 322      41.912  11.872  16.840  1.00 18.99
ATOM   2071  CE2 PHE A 322      41.535  11.229  14.552  1.00 17.99
ATOM   2072  CZ  PHE A 322      41.829  12.210  15.494  1.00 16.28
ATOM   2073  N   TRP A 323      38.367   8.063  15.552  1.00 20.75
ATOM   2074  CA  TRP A 323      37.330   8.622  14.664  1.00 22.37
ATOM   2075  C   TRP A 323      35.940   8.626  15.273  1.00 23.50
ATOM   2076  O   TRP A 323      35.036   9.379  14.804  1.00 22.84
ATOM   2077  CB  TRP A 323      37.322   7.872  13.335  1.00 21.45
ATOM   2078  CG  TRP A 323      38.643   7.924  12.664  1.00 20.71
ATOM   2079  CD1 TRP A 323      39.566   6.921  12.594  1.00 20.50
ATOM   2080  CD2 TRP A 323      39.217   9.049  11.986  1.00 20.31
ATOM   2081  NE1 TRP A 323      40.679   7.349  11.913  1.00 20.18
ATOM   2082  CE2 TRP A 323      40.492   8.651  11.527  1.00 20.95
ATOM   2083  CE3 TRP A 323      38.778  10.354  11.722  1.00 20.80
ATOM   2084  CZ2 TRP A 323      41.337   9.511  10.816  1.00 20.49
ATOM   2085  CZ3 TRP A 323      39.618  11.212  11.013  1.00 21.58
ATOM   2086  CH2 TRP A 323      40.885  10.784  10.569  1.00 21.15
ATOM   2087  N   LEU A 324      35.734   7.810  16.300  1.00 26.13
ATOM   2088  CA  LEU A 324      34.428   7.772  16.983  1.00 27.96
ATOM   2089  C   LEU A 324      34.417   8.877  18.040  1.00 29.09
ATOM   2090  O   LEU A 324      33.413   9.044  18.799  1.00 29.23
ATOM   2091  CB  LEU A 324      34.202   6.408  17.642  1.00 29.11
ATOM   2092  CG  LEU A 324      33.910   5.236  16.697  1.00 30.04
ATOM   2093  CD1 LEU A 324      33.791   3.948  17.501  1.00 30.31
ATOM   2094  CD2 LEU A 324      32.625   5.499  15.924  1.00 29.47
ATOM   2095  N   GLY A 325      35.513   9.634  18.098  1.00 29.34
ATOM   2096  CA  GLY A 325      35.632  10.728  19.048  1.00 30.68
ATOM   2097  C   GLY A 325      35.794  10.280  20.489  1.00 31.19
ATOM   2098  O   GLY A 325      35.687  11.109  21.442  1.00 31.53
ATOM   2099  N   GLU A 326      36.067   8.995  20.683  1.00 32.22
ATOM   2100  CA  GLU A 326      36.225   8.436  22.042  1.00 34.09
ATOM   2101  C   GLU A 326      37.655   8.482  22.563  1.00 33.56
ATOM   2102  O   GLU A 326      37.907   8.933  23.720  1.00 34.19
ATOM   2103  CB  GLU A 326      35.728   6.992  22.062  1.00 35.56
ATOM   2104  CG  GLU A 326      34.267   6.847  21.683  1.00 38.03
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ATOM   2105  CD  GLU A 326      33.855   5.401  21.494  1.00 40.36
ATOM   2106  OE1 GLU A 326      32.662   5.162  21.207  1.00 41.84
ATOM   2107  OE2 GLU A 326      34.720   4.506  21.626  1.00 42.10
ATOM   2108  N   GLN A 327      38.602   8.031  21.750  1.00 32.81
ATOM   2109  CA  GLN A 327      40.009   8.017  22.178  1.00 31.36
ATOM   2110  C   GLN A 327      40.844   9.142  21.608  1.00 30.14
ATOM   2111  O   GLN A 327      40.612   9.626  20.458  1.00 28.97
ATOM   2112  CB  GLN A 327      40.650   6.667  21.842  1.00 34.41
ATOM   2113  CG  GLN A 327      40.770   5.749  23.060  1.00 38.96
ATOM   2114  CD  GLN A 327      39.443   5.546  23.778  1.00 40.61
ATOM   2115  OE1 GLN A 327      39.410   5.223  25.002  1.00 42.73
ATOM   2116  NE2 GLN A 327      38.344   5.714  23.053  1.00 42.75
ATOM   2117  N   LEU A 328      41.814   9.581  22.394  1.00 28.01
ATOM   2118  CA  LEU A 328      42.695  10.663  21.964  1.00 28.64
ATOM   2119  C   LEU A 328      43.889  10.100  21.219  1.00 27.50
ATOM   2120  O   LEU A 328      44.207   8.873  21.317  1.00 27.23
ATOM   2121  CB  LEU A 328      43.177  11.467  23.180  1.00 29.39
ATOM   2122  CG  LEU A 328      43.924  10.735  24.304  1.00 31.09
ATOM   2123  CD1 LEU A 328      45.298  10.283  23.831  1.00 31.75
ATOM   2124  CD2 LEU A 328      44.074  11.669  25.498  1.00 31.12
ATOM   2125  N   VAL A 329      44.539  10.961  20.449  1.00 25.26
ATOM   2126  CA  VAL A 329      45.748  10.583  19.722  1.00 23.64
ATOM   2127  C   VAL A 329      46.779  11.593  20.203  1.00 23.76
ATOM   2128  O   VAL A 329      46.431  12.786  20.476  1.00 21.96
ATOM   2129  CB  VAL A 329      45.560  10.675  18.194  1.00 23.82
ATOM   2130  CG1 VAL A 329      45.100  12.070  17.794  1.00 23.64
ATOM   2131  CG2 VAL A 329      46.866  10.317  17.501  1.00 23.70
ATOM   2132  N   CYS A 330      48.025  11.157  20.344  1.00 23.69
ATOM   2133  CA  CYS A 330      49.088  12.046  20.830  1.00 24.17
ATOM   2134  C   CYS A 330      50.315  12.060  19.937  1.00 23.87
ATOM   2135  O   CYS A 330      50.592  11.089  19.165  1.00 24.32
ATOM   2136  CB  CYS A 330      49.548  11.633  22.228  1.00 24.93
ATOM   2137  SG  CYS A 330      48.353  11.638  23.608  1.00 29.07
ATOM   2138  N   TRP A 331      51.069  13.144  20.047  1.00 22.66
ATOM   2139  CA  TRP A 331      52.306  13.318  19.281  1.00 22.40
ATOM   2140  C   TRP A 331      53.333  13.972  20.177  1.00 22.22
ATOM   2141  O   TRP A 331      52.979  14.698  21.154  1.00 21.57
ATOM   2142  CB  TRP A 331      52.069  14.207  18.064  1.00 21.16
ATOM   2143  CG  TRP A 331      51.345  13.524  16.959  1.00 19.61
ATOM   2144  CD1 TRP A 331      51.868  12.634  16.067  1.00 18.33
ATOM   2145  CD2 TRP A 331      49.966  13.684  16.606  1.00 18.42
ATOM   2146  NE1 TRP A 331      50.902  12.233  15.177  1.00 17.37
ATOM   2147  CE2 TRP A 331      49.721  12.862  15.488  1.00 18.60
ATOM   2148  CE3 TRP A 331      48.911  14.446  17.130  1.00 19.20
ATOM   2149  CZ2 TRP A 331      48.467  12.778  14.874  1.00 17.86
ATOM   2150  CZ3 TRP A 331      47.659  14.364  16.521  1.00 19.94
ATOM   2151  CH2 TRP A 331      47.450  13.535  15.406  1.00 19.08
ATOM   2152  N   GLN A 332      54.598  13.730  19.873  1.00 23.04
ATOM   2153  CA  GLN A 332      55.689  14.321  20.648  1.00 25.14
ATOM   2154  C   GLN A 332      55.490  15.836  20.594  1.00 23.64
ATOM   2155  O   GLN A 332      55.066  16.397  19.533  1.00 23.11
ATOM   2156  CB  GLN A 332      57.020  13.937  20.015  1.00 27.80
ATOM   2157  CG  GLN A 332      58.171  13.877  20.982  1.00 33.30
ATOM   2158  CD  GLN A 332      59.450  13.445  20.305  1.00 35.55
ATOM   2159  OE1 GLN A 332      60.060  14.224  19.507  1.00 36.94
ATOM   2160  NE2 GLN A 332      59.879  12.217  20.579  1.00 36.57
ATOM   2161  N   ALA A 333      55.778  16.506  21.704  1.00 22.79
ATOM   2162  CA  ALA A 333      55.618  17.977  21.820  1.00 21.04
ATOM   2163  C   ALA A 333      55.936  18.759  20.552  1.00 19.77
ATOM   2164  O   ALA A 333      57.076  18.671  19.997  1.00 19.85
ATOM   2165  CB  ALA A 333      56.475  18.499  22.971  1.00 21.00
ATOM   2166  N   GLY A 334      54.949  19.515  20.083  1.00 17.64
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ATOM   2167  CA  GLY A 334      55.123  20.340  18.903  1.00 16.89
ATOM   2168  C   GLY A 334      55.205  19.663  17.548  1.00 17.61
ATOM   2169  O   GLY A 334      55.403  20.370  16.512  1.00 17.50
ATOM   2170  N   THR A 335      55.060  18.343  17.490  1.00 16.55
ATOM   2171  CA  THR A 335      55.146  17.648  16.182  1.00 17.58
ATOM   2172  C   THR A 335      53.802  17.260  15.557  1.00 16.83
ATOM   2173  O   THR A 335      53.761  16.408  14.618  1.00 17.71
ATOM   2174  CB  THR A 335      56.017  16.377  16.275  1.00 17.76
ATOM   2175  OG1 THR A 335      55.361  15.401  17.095  1.00 17.56
ATOM   2176  CG2 THR A 335      57.373  16.710  16.884  1.00 17.23
ATOM   2177  N   THR A 336      52.707  17.842  16.037  1.00 16.75
ATOM   2178  CA  THR A 336      51.373  17.527  15.460  1.00 16.56
ATOM   2179  C   THR A 336      51.473  17.752  13.952  1.00 16.24
ATOM   2180  O   THR A 336      51.821  18.868  13.487  1.00 16.30
ATOM   2181  CB  THR A 336      50.267  18.437  16.030  1.00 17.05
ATOM   2182  OG1 THR A 336      50.181  18.255  17.451  1.00 17.15
ATOM   2183  CG2 THR A 336      48.917  18.096  15.401  1.00 16.72
ATOM   2184  N   PRO A 337      51.182  16.718  13.157  1.00 15.50
ATOM   2185  CA  PRO A 337      51.254  16.820  11.699  1.00 14.87
ATOM   2186  C   PRO A 337      50.006  17.444  11.082  1.00 14.56
ATOM   2187  O   PRO A 337      49.310  16.800  10.249  1.00 14.49
ATOM   2188  CB  PRO A 337      51.448  15.369  11.281  1.00 15.18
ATOM   2189  CG  PRO A 337      50.520  14.657  12.238  1.00 16.05
ATOM   2190  CD  PRO A 337      50.784  15.359  13.572  1.00 15.54
ATOM   2191  N   TRP A 338      49.713  18.682  11.470  1.00 14.89
ATOM   2192  CA  TRP A 338      48.535  19.415  10.956  1.00 14.85
ATOM   2193  C   TRP A 338      48.339  19.304   9.445  1.00 14.87
ATOM   2194  O   TRP A 338      47.194  19.048   8.966  1.00 17.13
ATOM   2195  CB  TRP A 338      48.639  20.899  11.313  1.00 13.77
ATOM   2196  CG  TRP A 338      48.784  21.176  12.767  1.00 15.11
ATOM   2197  CD1 TRP A 338      49.897  21.652  13.411  1.00 14.78
ATOM   2198  CD2 TRP A 338      47.780  21.011  13.771  1.00 14.17
ATOM   2199  NE1 TRP A 338      49.641  21.794  14.756  1.00 14.64
ATOM   2200  CE2 TRP A 338      48.348  21.407  15.003  1.00 14.35
ATOM   2201  CE3 TRP A 338      46.451  20.566  13.751  1.00 14.31
ATOM   2202  CZ2 TRP A 338      47.635  21.371  16.202  1.00 14.86
ATOM   2203  CZ3 TRP A 338      45.744  20.530  14.945  1.00 16.02
ATOM   2204  CH2 TRP A 338      46.339  20.932  16.154  1.00 14.77
ATOM   2205  N   ASN A 339      49.414  19.486   8.682  1.00 13.22
ATOM   2206  CA  ASN A 339      49.319  19.449   7.203  1.00 12.87
ATOM   2207  C   ASN A 339      48.674  18.208   6.608  1.00 12.01
ATOM   2208  O   ASN A 339      48.061  18.288   5.508  1.00 13.99
ATOM   2209  CB  ASN A 339      50.699  19.649   6.552  1.00 12.61
ATOM   2210  CG  ASN A 339      51.576  18.404   6.627  1.00 15.28
ATOM   2211  OD1 ASN A 339      52.290  18.174   7.648  1.00 16.29
ATOM   2212  ND2 ASN A 339      51.541  17.584   5.578  1.00 12.93
ATOM   2213  N   ILE A 340      48.774  17.064   7.276  1.00 12.88
ATOM   2214  CA  ILE A 340      48.171  15.831   6.698  1.00 12.98
ATOM   2215  C   ILE A 340      46.655  15.864   6.794  1.00 12.80
ATOM   2216  O   ILE A 340      45.944  15.237   5.959  1.00 12.80
ATOM   2217  CB  ILE A 340      48.667  14.545   7.400  1.00 14.79
ATOM   2218  CG1 ILE A 340      48.142  14.512   8.833  1.00 14.91
ATOM   2219  CG2 ILE A 340      50.194  14.483   7.372  1.00 12.38
ATOM   2220  CD1 ILE A 340      48.177  13.142   9.454  1.00 17.42
ATOM   2221  N   PHE A 341      46.138  16.577   7.790  1.00 13.19
ATOM   2222  CA  PHE A 341      44.677  16.689   7.972  1.00 13.87
ATOM   2223  C   PHE A 341      44.143  17.741   7.006  1.00 13.37
ATOM   2224  O   PHE A 341      44.787  18.812   6.798  1.00 12.72
ATOM   2225  CB  PHE A 341      44.354  17.087   9.410  1.00 13.10
ATOM   2226  CG  PHE A 341      44.685  16.027  10.429  1.00 13.55
ATOM   2227  CD1 PHE A 341      43.817  14.960  10.654  1.00 13.48
ATOM   2228  CD2 PHE A 341      45.861  16.104  11.171  1.00 12.12
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ATOM   2229  CE1 PHE A 341      44.115  13.984  11.607  1.00 13.44
ATOM   2230  CE2 PHE A 341      46.172  15.136  12.127  1.00 14.31
ATOM   2231  CZ  PHE A 341      45.298  14.074  12.346  1.00 13.92
ATOM   2232  N   PRO A 342      42.975  17.484   6.402  1.00 12.78
ATOM   2233  CA  PRO A 342      42.357  18.413   5.448  1.00 12.17
ATOM   2234  C   PRO A 342      41.565  19.544   6.100  1.00 12.90
ATOM   2235  O   PRO A 342      41.168  19.465   7.309  1.00 12.52
ATOM   2236  CB  PRO A 342      41.447  17.502   4.638  1.00 10.18
ATOM   2237  CG  PRO A 342      40.920  16.570   5.714  1.00 11.48
ATOM   2238  CD  PRO A 342      42.180  16.244   6.523  1.00 12.10
ATOM   2239  N   VAL A 343      41.342  20.609   5.342  1.00 12.27
ATOM   2240  CA  VAL A 343      40.528  21.712   5.851  1.00 10.51
ATOM   2241  C   VAL A 343      39.101  21.281   5.521  1.00 12.41
ATOM   2242  O   VAL A 343      38.878  20.401   4.632  1.00 10.45
ATOM   2243  CB  VAL A 343      40.838  23.054   5.143  1.00 10.23
ATOM   2244  CG1 VAL A 343      42.247  23.507   5.488  1.00  8.58
ATOM   2245  CG2 VAL A 343      40.672  22.914   3.636  1.00  8.08
ATOM   2246  N   ILE A 344      38.132  21.848   6.224  1.00 13.49
ATOM   2247  CA  ILE A 344      36.725  21.507   5.991  1.00 13.17
ATOM   2248  C   ILE A 344      35.989  22.789   5.664  1.00 13.33
ATOM   2249  O   ILE A 344      36.067  23.795   6.427  1.00 13.12
ATOM   2250  CB  ILE A 344      36.099  20.859   7.246  1.00 14.77
ATOM   2251  CG1 ILE A 344      36.776  19.512   7.517  1.00 14.50
ATOM   2252  CG2 ILE A 344      34.585  20.702   7.060  1.00 13.14
ATOM   2253  CD1 ILE A 344      36.374  18.875   8.825  1.00 17.73
ATOM   2254  N   SER A 345      35.292  22.794   4.537  1.00 12.41
ATOM   2255  CA  SER A 345      34.547  23.982   4.136  1.00 13.41
ATOM   2256  C   SER A 345      33.051  23.723   4.172  1.00 14.94
ATOM   2257  O   SER A 345      32.555  22.641   3.721  1.00 14.55
ATOM   2258  CB  SER A 345      34.967  24.430   2.728  1.00 14.23
ATOM   2259  OG  SER A 345      36.329  24.834   2.703  1.00 13.57
ATOM   2260  N   LEU A 346      32.320  24.682   4.725  1.00 13.42
ATOM   2261  CA  LEU A 346      30.859  24.594   4.796  1.00 14.08
ATOM   2262  C   LEU A 346      30.320  25.772   4.003  1.00 13.86
ATOM   2263  O   LEU A 346      30.681  26.956   4.286  1.00 13.52
ATOM   2264  CB  LEU A 346      30.383  24.674   6.252  1.00 15.83
ATOM   2265  CG  LEU A 346      30.239  23.372   7.051  1.00 17.74
ATOM   2266  CD1 LEU A 346      31.455  22.492   6.875  1.00 18.92
ATOM   2267  CD2 LEU A 346      30.028  23.711   8.521  1.00 19.69
ATOM   2268  N   TYR A 347      29.496  25.485   3.000  1.00 13.48
ATOM   2269  CA  TYR A 347      28.894  26.543   2.176  1.00 13.76
ATOM   2270  C   TYR A 347      27.525  26.864   2.745  1.00 14.58
ATOM   2271  O   TYR A 347      26.676  25.948   2.979  1.00 13.16
ATOM   2272  CB  TYR A 347      28.757  26.101   0.716  1.00 14.82
ATOM   2273  CG  TYR A 347      30.066  26.051  -0.034  1.00 15.10
ATOM   2274  CD1 TYR A 347      31.022  25.074   0.252  1.00 13.97
ATOM   2275  CD2 TYR A 347      30.349  26.977  -1.038  1.00 13.98
ATOM   2276  CE1 TYR A 347      32.228  25.018  -0.447  1.00 14.47
ATOM   2277  CE2 TYR A 347      31.556  26.930  -1.746  1.00 15.69
ATOM   2278  CZ  TYR A 347      32.487  25.949  -1.445  1.00 15.09
ATOM   2279  OH  TYR A 347      33.672  25.895  -2.141  1.00 16.72
ATOM   2280  N   LEU A 348      27.288  28.145   2.971  1.00 13.86
ATOM   2281  CA  LEU A 348      26.018  28.593   3.545  1.00 16.70
ATOM   2282  C   LEU A 348      25.246  29.445   2.559  1.00 17.37
ATOM   2283  O   LEU A 348      25.856  30.183   1.722  1.00 16.05
ATOM   2284  CB  LEU A 348      26.292  29.401   4.814  1.00 15.57
ATOM   2285  CG  LEU A 348      27.019  28.620   5.908  1.00 17.10
ATOM   2286  CD1 LEU A 348      27.518  29.565   6.985  1.00 15.71
ATOM   2287  CD2 LEU A 348      26.078  27.580   6.495  1.00 16.92
ATOM   2288  N   MET A 349      23.922  29.352   2.617  1.00 19.68
ATOM   2289  CA  MET A 349      23.073  30.167   1.734  1.00 22.78
ATOM   2290  C   MET A 349      23.384  31.629   2.024  1.00 22.03
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ATOM   2291  O   MET A 349      23.478  32.049   3.222  1.00 20.70
ATOM   2292  CB  MET A 349      21.594  29.897   2.008  1.00 25.40
ATOM   2293  CG  MET A 349      20.931  28.954   1.012  1.00 31.18
ATOM   2294  SD  MET A 349      19.139  28.833   1.272  1.00 37.43
ATOM   2295  CE  MET A 349      18.697  30.583   1.318  1.00 32.73
ATOM   2296  N   GLY A 350      23.573  32.414   0.972  1.00 20.81
ATOM   2297  CA  GLY A 350      23.857  33.824   1.167  1.00 23.50
ATOM   2298  C   GLY A 350      22.565  34.612   1.280  1.00 24.26
ATOM   2299  O   GLY A 350      21.450  34.042   1.091  1.00 23.13
ATOM   2300  N   GLU A 351      22.662  35.899   1.591  1.00 27.25
ATOM   2301  CA  GLU A 351      21.448  36.734   1.698  1.00 32.00
ATOM   2302  C   GLU A 351      20.870  36.948   0.306  1.00 33.92
ATOM   2303  O   GLU A 351      19.620  37.066   0.125  1.00 34.42
ATOM   2304  CB  GLU A 351      21.774  38.081   2.340  1.00 32.31
ATOM   2305  CG  GLU A 351      22.012  37.996   3.831  1.00 34.92
ATOM   2306  CD  GLU A 351      21.916  39.346   4.503  1.00 35.55
ATOM   2307  OE1 GLU A 351      22.819  40.187   4.293  1.00 36.64
ATOM   2308  OE2 GLU A 351      20.927  39.567   5.233  1.00 36.29
ATOM   2309  N   VAL A 352      21.753  37.007  -0.684  1.00 36.98
ATOM   2310  CA  VAL A 352      21.327  37.181  -2.082  1.00 38.72
ATOM   2311  C   VAL A 352      20.944  35.809  -2.629  1.00 40.47
ATOM   2312  O   VAL A 352      21.689  34.799  -2.426  1.00 39.68
ATOM   2313  CB  VAL A 352      22.456  37.767  -2.939  1.00 38.31
ATOM   2314  CG1 VAL A 352      21.999  37.892  -4.382  1.00 38.33
ATOM   2315  CG2 VAL A 352      22.866  39.123  -2.391  1.00 37.93
ATOM   2316  N   THR A 353      19.806  35.747  -3.314  1.00 42.33
ATOM   2317  CA  THR A 353      19.300  34.476  -3.882  1.00 43.97
ATOM   2318  C   THR A 353      20.254  33.832  -4.877  1.00 43.18
ATOM   2319  O   THR A 353      20.941  34.536  -5.688  1.00 42.65
ATOM   2320  CB  THR A 353      17.929  34.672  -4.578  1.00 45.29
ATOM   2321  OG1 THR A 353      18.018  35.743  -5.526  1.00 46.63
ATOM   2322  CG2 THR A 353      16.849  34.988  -3.551  1.00 46.31
ATOM   2323  N   ASN A 354      20.307  32.507  -4.839  1.00 42.20
ATOM   2324  CA  ASN A 354      21.183  31.741  -5.742  1.00 43.39
ATOM   2325  C   ASN A 354      22.641  32.166  -5.611  1.00 41.22
ATOM   2326  O   ASN A 354      23.444  32.078  -6.584  1.00 43.04
ATOM   2327  CB  ASN A 354      20.698  31.887  -7.187  1.00 45.64
ATOM   2328  CG  ASN A 354      19.467  31.036  -7.474  1.00 47.44
ATOM   2329  OD1 ASN A 354      18.824  31.163  -8.562  1.00 48.61
ATOM   2330  ND2 ASN A 354      19.121  30.159  -6.534  1.00 47.73
ATOM   2331  N   GLN A 355      22.999  32.621  -4.419  1.00 37.62
ATOM   2332  CA  GLN A 355      24.371  33.042  -4.128  1.00 34.85
ATOM   2333  C   GLN A 355      24.737  32.475  -2.764  1.00 32.57
ATOM   2334  O   GLN A 355      23.863  32.388  -1.846  1.00 31.25
ATOM   2335  CB  GLN A 355      24.459  34.563  -4.105  1.00 35.77
ATOM   2336  CG  GLN A 355      25.834  35.089  -3.797  1.00 38.04
ATOM   2337  CD  GLN A 355      25.909  36.590  -3.915  1.00 39.05
ATOM   2338  OE1 GLN A 355      25.586  37.171  -4.992  1.00 40.57
ATOM   2339  NE2 GLN A 355      26.331  37.249  -2.844  1.00 39.68
ATOM   2340  N   SER A 356      25.989  32.071  -2.597  1.00 29.33
ATOM   2341  CA  SER A 356      26.419  31.514  -1.304  1.00 25.60
ATOM   2342  C   SER A 356      27.850  31.897  -0.981  1.00 22.66
ATOM   2343  O   SER A 356      28.580  32.481  -1.833  1.00 21.99
ATOM   2344  CB  SER A 356      26.313  29.991  -1.318  1.00 25.71
ATOM   2345  OG  SER A 356      27.449  29.425  -1.945  1.00 24.59
ATOM   2346  N   PHE A 357      28.267  31.583   0.239  1.00 20.53
ATOM   2347  CA  PHE A 357      29.639  31.865   0.676  1.00 17.95
ATOM   2348  C   PHE A 357      30.104  30.643   1.437  1.00 17.15
ATOM   2349  O   PHE A 357      29.279  29.750   1.784  1.00 17.21
ATOM   2350  CB  PHE A 357      29.687  33.126   1.550  1.00 17.62
ATOM   2351  CG  PHE A 357      28.926  33.017   2.850  1.00 17.61
ATOM   2352  CD1 PHE A 357      29.571  32.625   4.018  1.00 15.09
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ATOM   2353  CD2 PHE A 357      27.577  33.357   2.912  1.00 16.90
ATOM   2354  CE1 PHE A 357      28.887  32.577   5.229  1.00 14.87
ATOM   2355  CE2 PHE A 357      26.881  33.312   4.120  1.00 15.64
ATOM   2356  CZ  PHE A 357      27.538  32.924   5.280  1.00 16.14
ATOM   2357  N   ARG A 358      31.397  30.545   1.687  1.00 16.29
ATOM   2358  CA  ARG A 358      31.891  29.383   2.412  1.00 14.04
ATOM   2359  C   ARG A 358      32.642  29.755   3.664  1.00 14.59
ATOM   2360  O   ARG A 358      33.237  30.869   3.785  1.00 13.01
ATOM   2361  CB  ARG A 358      32.784  28.525   1.516  1.00 14.11
ATOM   2362  CG  ARG A 358      34.084  29.172   1.102  1.00 13.28
ATOM   2363  CD  ARG A 358      34.809  28.275   0.121  1.00 13.06
ATOM   2364  NE  ARG A 358      36.090  28.831  -0.291  1.00 14.39
ATOM   2365  CZ  ARG A 358      36.723  28.489  -1.409  1.00 14.92
ATOM   2366  NH1 ARG A 358      36.188  27.591  -2.232  1.00 13.71
ATOM   2367  NH2 ARG A 358      37.888  29.045  -1.701  1.00 12.88
ATOM   2368  N   ILE A 359      32.612  28.819   4.596  1.00 14.51
ATOM   2369  CA  ILE A 359      33.268  28.935   5.891  1.00 16.36
ATOM   2370  C   ILE A 359      34.242  27.762   5.913  1.00 15.41
ATOM   2371  O   ILE A 359      33.836  26.583   5.675  1.00 15.49
ATOM   2372  CB  ILE A 359      32.197  28.824   7.001  1.00 17.94
ATOM   2373  CG1 ILE A 359      31.543  30.190   7.198  1.00 19.68
ATOM   2374  CG2 ILE A 359      32.766  28.260   8.255  1.00 20.12
ATOM   2375  CD1 ILE A 359      32.515  31.288   7.500  1.00 22.40
ATOM   2376  N   THR A 360      35.513  28.046   6.162  1.00 13.01
ATOM   2377  CA  THR A 360      36.531  26.983   6.167  1.00 14.32
ATOM   2378  C   THR A 360      37.307  26.894   7.470  1.00 14.04
ATOM   2379  O   THR A 360      37.892  27.913   7.938  1.00 13.82
ATOM   2380  CB  THR A 360      37.536  27.202   5.021  1.00 14.49
ATOM   2381  OG1 THR A 360      36.828  27.286   3.774  1.00 15.69
ATOM   2382  CG2 THR A 360      38.532  26.053   4.964  1.00 15.11
ATOM   2383  N   ILE A 361      37.331  25.709   8.074  1.00 13.79
ATOM   2384  CA  ILE A 361      38.091  25.524   9.330  1.00 17.36
ATOM   2385  C   ILE A 361      39.241  24.548   9.122  1.00 16.53
ATOM   2386  O   ILE A 361      39.237  23.717   8.160  1.00 16.37
ATOM   2387  CB  ILE A 361      37.208  24.982  10.476  1.00 18.15
ATOM   2388  CG1 ILE A 361      36.608  23.632  10.077  1.00 18.53
ATOM   2389  CG2 ILE A 361      36.126  25.999  10.830  1.00 18.95
ATOM   2390  CD1 ILE A 361      35.899  22.937  11.208  1.00 18.19
ATOM   2391  N   LEU A 362      40.230  24.614   9.998  1.00 17.82
ATOM   2392  CA  LEU A 362      41.375  23.710   9.876  1.00 18.92
ATOM   2393  C   LEU A 362      41.412  22.659  10.983  1.00 17.87
ATOM   2394  O   LEU A 362      40.533  22.654  11.912  1.00 17.21
ATOM   2395  CB  LEU A 362      42.675  24.525   9.837  1.00 22.47
ATOM   2396  CG  LEU A 362      42.686  25.974  10.320  1.00 25.03
ATOM   2397  CD1 LEU A 362      42.945  25.992  11.802  1.00 28.14
ATOM   2398  CD2 LEU A 362      43.781  26.751   9.623  1.00 25.06
ATOM   2399  N   PRO A 363      42.380  21.729  10.910  1.00 16.12
ATOM   2400  CA  PRO A 363      42.507  20.681  11.925  1.00 14.51
ATOM   2401  C   PRO A 363      42.628  21.325  13.303  1.00 14.50
ATOM   2402  O   PRO A 363      42.234  20.710  14.339  1.00 13.48
ATOM   2403  CB  PRO A 363      43.801  19.971  11.534  1.00 15.57
ATOM   2404  CG  PRO A 363      43.902  20.202  10.076  1.00 16.87
ATOM   2405  CD  PRO A 363      43.450  21.616   9.903  1.00 14.60
ATOM   2406  N   GLN A 364      43.178  22.539  13.337  1.00 12.36
ATOM   2407  CA  GLN A 364      43.357  23.271  14.608  1.00 13.04
ATOM   2408  C   GLN A 364      42.014  23.557  15.254  1.00 13.41
ATOM   2409  O   GLN A 364      41.953  23.895  16.467  1.00 12.73
ATOM   2410  CB  GLN A 364      44.111  24.585  14.392  1.00 12.04
ATOM   2411  CG  GLN A 364      45.637  24.449  14.304  1.00 11.85
ATOM   2412  CD  GLN A 364      46.141  24.079  12.919  1.00 11.11
ATOM   2413  OE1 GLN A 364      47.372  24.211  12.625  1.00 13.65
ATOM   2414  NE2 GLN A 364      45.245  23.621  12.056  1.00  8.04
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ATOM   2415  N   GLN A 365      40.939  23.446  14.478  1.00 13.30
ATOM   2416  CA  GLN A 365      39.580  23.657  15.023  1.00 14.36
ATOM   2417  C   GLN A 365      38.873  22.341  15.339  1.00 14.57
ATOM   2418  O   GLN A 365      38.312  22.175  16.457  1.00 16.56
ATOM   2419  CB  GLN A 365      38.691  24.452  14.056  1.00 14.03
ATOM   2420  CG  GLN A 365      38.816  25.962  14.167  1.00 15.23
ATOM   2421  CD  GLN A 365      40.073  26.489  13.515  1.00 15.81
ATOM   2422  OE1 GLN A 365      40.290  26.292  12.282  1.00 15.51
ATOM   2423  NE2 GLN A 365      40.917  27.158  14.295  1.00 15.82
ATOM   2424  N   TYR A 366      38.873  21.392  14.406  1.00 14.93
ATOM   2425  CA  TYR A 366      38.149  20.128  14.673  1.00 15.12
ATOM   2426  C   TYR A 366      38.914  19.053  15.447  1.00 15.66
ATOM   2427  O   TYR A 366      38.378  17.930  15.703  1.00 17.42
ATOM   2428  CB  TYR A 366      37.557  19.567  13.371  1.00 14.28
ATOM   2429  CG  TYR A 366      38.541  19.107  12.322  1.00 13.05
ATOM   2430  CD1 TYR A 366      39.228  17.907  12.467  1.00 13.67
ATOM   2431  CD2 TYR A 366      38.721  19.835  11.145  1.00 13.44
ATOM   2432  CE1 TYR A 366      40.062  17.431  11.463  1.00 12.91
ATOM   2433  CE2 TYR A 366      39.555  19.369  10.128  1.00 12.63
ATOM   2434  CZ  TYR A 366      40.218  18.163  10.294  1.00 13.86
ATOM   2435  OH  TYR A 366      41.008  17.669   9.287  1.00 12.42
ATOM   2436  N   LEU A 367      40.144  19.367  15.835  1.00 16.84
ATOM   2437  CA  LEU A 367      40.966  18.450  16.660  1.00 16.98
ATOM   2438  C   LEU A 367      40.996  19.161  18.017  1.00 17.50
ATOM   2439  O   LEU A 367      41.662  20.224  18.172  1.00 16.40
ATOM   2440  CB  LEU A 367      42.382  18.324  16.088  1.00 17.44
ATOM   2441  CG  LEU A 367      42.764  16.991  15.429  1.00 18.54
ATOM   2442  CD1 LEU A 367      41.681  16.534  14.482  1.00 17.60
ATOM   2443  CD2 LEU A 367      44.091  17.143  14.700  1.00 17.38
ATOM   2444  N   ARG A 368      40.270  18.624  18.990  1.00 17.06
ATOM   2445  CA  ARG A 368      40.192  19.253  20.326  1.00 17.22
ATOM   2446  C   ARG A 368      41.341  18.874  21.243  1.00 16.52
ATOM   2447  O   ARG A 368      41.554  17.662  21.538  1.00 16.19
ATOM   2448  CB  ARG A 368      38.879  18.871  21.009  1.00 16.02
ATOM   2449  CG  ARG A 368      38.050  20.055  21.444  1.00 19.09
ATOM   2450  CD  ARG A 368      37.415  19.811  22.792  1.00 17.88
ATOM   2451  NE  ARG A 368      36.840  18.474  22.906  1.00 17.20
ATOM   2452  CZ  ARG A 368      36.775  17.806  24.053  1.00 18.65
ATOM   2453  NH1 ARG A 368      37.247  18.361  25.164  1.00 18.77
ATOM   2454  NH2 ARG A 368      36.258  16.584  24.095  1.00 17.53
ATOM   2455  N   PRO A 369      42.100  19.867  21.722  1.00 17.88
ATOM   2456  CA  PRO A 369      43.220  19.558  22.615  1.00 19.69
ATOM   2457  C   PRO A 369      42.744  19.067  23.969  1.00 22.16
ATOM   2458  O   PRO A 369      41.786  19.645  24.575  1.00 20.49
ATOM   2459  CB  PRO A 369      43.983  20.883  22.700  1.00 20.03
ATOM   2460  CG  PRO A 369      42.932  21.911  22.429  1.00 19.96
ATOM   2461  CD  PRO A 369      42.122  21.285  21.320  1.00 17.42
ATOM   2462  N   VAL A 370      43.376  18.001  24.444  1.00 23.75
ATOM   2463  CA  VAL A 370      43.040  17.399  25.747  1.00 27.84
ATOM   2464  C   VAL A 370      44.332  16.921  26.394  1.00 30.26
ATOM   2465  O   VAL A 370      45.321  16.577  25.682  1.00 30.79
ATOM   2466  CB  VAL A 370      42.093  16.197  25.577  1.00 26.52
ATOM   2467  CG1 VAL A 370      40.771  16.654  24.989  1.00 26.57
ATOM   2468  CG2 VAL A 370      42.737  15.160  24.669  1.00 26.53
ATOM   2469  N   GLU A 371      44.361  16.891  27.719  1.00 35.50
ATOM   2470  CA  GLU A 371      45.574  16.450  28.426  1.00 40.60
ATOM   2471  C   GLU A 371      45.800  14.963  28.235  1.00 42.42
ATOM   2472  O   GLU A 371      44.832  14.138  28.321  1.00 41.89
ATOM   2473  CB  GLU A 371      45.472  16.758  29.921  1.00 43.12
ATOM   2474  CG  GLU A 371      46.603  17.634  30.443  1.00 47.33
ATOM   2475  CD  GLU A 371      47.954  17.245  29.864  1.00 49.98
ATOM   2476  OE1 GLU A 371      48.264  16.036  29.818  1.00 51.63
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ATOM   2477  OE2 GLU A 371      48.710  18.151  29.456  1.00 51.00
ATOM   2478  N   ASP A 372      47.046  14.596  27.960  1.00 45.77
ATOM   2479  CA  ASP A 372      47.396  13.182  27.774  1.00 49.75
ATOM   2480  C   ASP A 372      46.889  12.468  29.014  1.00 52.41
ATOM   2481  O   ASP A 372      47.090  12.966  30.165  1.00 52.32
ATOM   2482  CB  ASP A 372      48.913  13.015  27.665  1.00 50.28
ATOM   2483  CG  ASP A 372      49.323  11.587  27.333  1.00 51.15
ATOM   2484  OD1 ASP A 372      50.541  11.323  27.246  1.00 51.32
ATOM   2485  OD2 ASP A 372      48.429  10.729  27.156  1.00 50.76
ATOM   2486  N   VAL A 373      46.217  11.340  28.819  1.00 55.35
ATOM   2487  CA  VAL A 373      45.688  10.570  29.956  1.00 58.73
ATOM   2488  C   VAL A 373      46.850  10.213  30.896  1.00 60.04
ATOM   2489  O   VAL A 373      47.465   9.105  30.817  1.00 60.06
ATOM   2490  CB  VAL A 373      44.901   9.313  29.433  1.00 59.43
ATOM   2491  CG1 VAL A 373      45.292   8.044  30.176  1.00 59.64
ATOM   2492  CG2 VAL A 373      43.402   9.556  29.597  1.00 59.89
ATOM   2493  N   ALA A 374      47.187  11.169  31.759  1.00 61.58
ATOM   2494  CA  ALA A 374      48.277  11.020  32.755  1.00 61.52
ATOM   2495  C   ALA A 374      49.709  11.205  32.233  1.00 61.38
ATOM   2496  O   ALA A 374      50.104  10.633  31.169  1.00 60.95
ATOM   2497  CB  ALA A 374      48.155   9.668  33.455  1.00 62.66
ATOM   2498  N   THR A 375      50.477  12.002  32.977  1.00 61.03
ATOM   2499  CA  THR A 375      51.919  12.320  32.715  1.00 60.30
ATOM   2500  C   THR A 375      52.401  12.358  31.269  1.00 58.41
ATOM   2501  O   THR A 375      52.361  11.308  30.555  1.00 59.21
ATOM   2502  CB  THR A 375      52.838  11.327  33.455  1.00 61.35
ATOM   2503  OG1 THR A 375      52.302  11.049  34.756  1.00 62.26
ATOM   2504  CG2 THR A 375      54.237  11.912  33.599  1.00 61.47
ATOM   2505  N   SER A 376      52.892  13.520  30.833  1.00 55.18
ATOM   2506  CA  SER A 376      53.407  13.683  29.445  1.00 51.40
ATOM   2507  C   SER A 376      53.538  15.132  28.981  1.00 48.79
ATOM   2508  O   SER A 376      52.887  16.067  29.540  1.00 48.19
ATOM   2509  CB  SER A 376      52.502  12.943  28.456  1.00 51.90
ATOM   2510  OG  SER A 376      52.880  13.193  27.115  1.00 51.94
ATOM   2511  N   GLN A 377      54.373  15.333  27.968  1.00 44.88
ATOM   2512  CA  GLN A 377      54.576  16.664  27.367  1.00 41.28
ATOM   2513  C   GLN A 377      54.106  16.580  25.923  1.00 37.22
ATOM   2514  O   GLN A 377      54.380  17.489  25.081  1.00 35.23
ATOM   2515  CB  GLN A 377      56.048  17.062  27.425  1.00 43.59
ATOM   2516  CG  GLN A 377      56.468  17.585  28.789  1.00 46.22
ATOM   2517  CD  GLN A 377      57.955  17.831  28.886  1.00 47.12
ATOM   2518  OE1 GLN A 377      58.710  17.710  27.867  1.00 48.44
ATOM   2519  NE2 GLN A 377      58.414  18.177  30.081  1.00 48.23
ATOM   2520  N   ASP A 378      53.399  15.499  25.618  1.00 31.89
ATOM   2521  CA  ASP A 378      52.866  15.289  24.263  1.00 28.31
ATOM   2522  C   ASP A 378      51.663  16.183  24.034  1.00 25.36
ATOM   2523  O   ASP A 378      50.958  16.590  25.004  1.00 22.58
ATOM   2524  CB  ASP A 378      52.422  13.835  24.072  1.00 28.64
ATOM   2525  CG  ASP A 378      53.582  12.867  23.998  1.00 29.19
ATOM   2526  OD1 ASP A 378      54.746  13.316  23.948  1.00 30.91
ATOM   2527  OD2 ASP A 378      53.323  11.647  23.981  1.00 30.50
ATOM   2528  N   ASP A 379      51.415  16.513  22.776  1.00 23.06
ATOM   2529  CA  ASP A 379      50.236  17.317  22.436  1.00 22.51
ATOM   2530  C   ASP A 379      49.220  16.294  21.964  1.00 21.46
ATOM   2531  O   ASP A 379      49.436  15.581  20.945  1.00 19.87
ATOM   2532  CB  ASP A 379      50.570  18.335  21.346  1.00 21.72
ATOM   2533  CG  ASP A 379      51.557  19.377  21.829  1.00 23.29
ATOM   2534  OD1 ASP A 379      51.434  19.786  23.005  1.00 23.00
ATOM   2535  OD2 ASP A 379      52.446  19.789  21.052  1.00 23.50
ATOM   2536  N   CYS A 380      48.128  16.182  22.706  1.00 20.99
ATOM   2537  CA  CYS A 380      47.082  15.201  22.393  1.00 20.40
ATOM   2538  C   CYS A 380      45.769  15.865  22.013  1.00 19.94
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ATOM   2539  O   CYS A 380      45.489  17.038  22.417  1.00 18.77
ATOM   2540  CB  CYS A 380      46.867  14.292  23.596  1.00 23.14
ATOM   2541  SG  CYS A 380      48.368  13.550  24.327  1.00 25.25
ATOM   2542  N   TYR A 381      44.947  15.140  21.255  1.00 18.49
ATOM   2543  CA  TYR A 381      43.656  15.681  20.785  1.00 17.31
ATOM   2544  C   TYR A 381      42.595  14.610  20.602  1.00 17.45
ATOM   2545  O   TYR A 381      42.890  13.376  20.532  1.00 16.46
ATOM   2546  CB  TYR A 381      43.833  16.370  19.427  1.00 15.47
ATOM   2547  CG  TYR A 381      45.034  17.275  19.314  1.00 14.93
ATOM   2548  CD1 TYR A 381      44.899  18.659  19.408  1.00 14.20
ATOM   2549  CD2 TYR A 381      46.311  16.746  19.118  1.00 14.17
ATOM   2550  CE1 TYR A 381      46.009  19.499  19.307  1.00 14.66
ATOM   2551  CE2 TYR A 381      47.431  17.576  19.021  1.00 15.73
ATOM   2552  CZ  TYR A 381      47.272  18.952  19.113  1.00 16.02
ATOM   2553  OH  TYR A 381      48.369  19.785  18.994  1.00 15.32
ATOM   2554  N   LYS A 382      41.356  15.066  20.506  1.00 18.35
ATOM   2555  CA  LYS A 382      40.218  14.174  20.248  1.00 20.26
ATOM   2556  C   LYS A 382      39.555  14.695  18.981  1.00 19.31
ATOM   2557  O   LYS A 382      39.575  15.941  18.704  1.00 19.65
ATOM   2558  CB  LYS A 382      39.221  14.204  21.404  1.00 21.74
ATOM   2559  CG  LYS A 382      39.632  13.348  22.585  1.00 25.42
ATOM   2560  CD  LYS A 382      38.509  13.266  23.602  1.00 27.59
ATOM   2561  CE  LYS A 382      38.878  12.342  24.759  1.00 29.84
ATOM   2562  NZ  LYS A 382      37.779  12.246  25.761  1.00 31.22
ATOM   2563  N   PHE A 383      38.994  13.786  18.192  1.00 18.55
ATOM   2564  CA  PHE A 383      38.298  14.165  16.942  1.00 16.97
ATOM   2565  C   PHE A 383      36.992  14.823  17.375  1.00 16.22
ATOM   2566  O   PHE A 383      36.079  14.138  17.908  1.00 13.73
ATOM   2567  CB  PHE A 383      38.026  12.907  16.110  1.00 16.57
ATOM   2568  CG  PHE A 383      37.447  13.182  14.750  1.00 16.49
ATOM   2569  CD1 PHE A 383      38.052  14.091  13.890  1.00 14.48
ATOM   2570  CD2 PHE A 383      36.319  12.489  14.308  1.00 15.06
ATOM   2571  CE1 PHE A 383      37.542  14.306  12.606  1.00 16.02
ATOM   2572  CE2 PHE A 383      35.807  12.696  13.029  1.00 15.64
ATOM   2573  CZ  PHE A 383      36.419  13.603  12.176  1.00 15.10
ATOM   2574  N   ALA A 384      36.885  16.134  17.173  1.00 16.28
ATOM   2575  CA  ALA A 384      35.675  16.893  17.586  1.00 15.54
ATOM   2576  C   ALA A 384      34.549  16.931  16.559  1.00 15.46
ATOM   2577  O   ALA A 384      33.768  17.931  16.487  1.00 15.60
ATOM   2578  CB  ALA A 384      36.061  18.316  17.987  1.00 14.96
ATOM   2579  N   ILE A 385      34.451  15.888  15.745  1.00 14.66
ATOM   2580  CA  ILE A 385      33.356  15.792  14.763  1.00 13.45
ATOM   2581  C   ILE A 385      32.651  14.487  15.093  1.00 14.39
ATOM   2582  O   ILE A 385      33.303  13.410  15.179  1.00 12.37
ATOM   2583  CB  ILE A 385      33.862  15.724  13.315  1.00 12.54
ATOM   2584  CG1 ILE A 385      34.696  16.959  12.988  1.00 13.08
ATOM   2585  CG2 ILE A 385      32.675  15.655  12.367  1.00 12.56
ATOM   2586  CD1 ILE A 385      35.178  17.003  11.549  1.00 10.74
ATOM   2587  N   SER A 386      31.343  14.543  15.297  1.00 14.95
ATOM   2588  CA  SER A 386      30.605  13.319  15.637  1.00 16.99
ATOM   2589  C   SER A 386      29.275  13.221  14.918  1.00 17.48
ATOM   2590  O   SER A 386      28.795  14.207  14.279  1.00 18.09
ATOM   2591  CB  SER A 386      30.385  13.240  17.151  1.00 16.69
ATOM   2592  OG  SER A 386      29.630  14.345  17.616  1.00 16.81
ATOM   2593  N   GLN A 387      28.673  12.044  15.016  1.00 19.86
ATOM   2594  CA  GLN A 387      27.384  11.748  14.376  1.00 23.09
ATOM   2595  C   GLN A 387      26.209  12.317  15.160  1.00 22.61
ATOM   2596  O   GLN A 387      26.221  12.363  16.427  1.00 22.90
ATOM   2597  CB  GLN A 387      27.222  10.234  14.247  1.00 24.53
ATOM   2598  CG  GLN A 387      26.035   9.795  13.411  1.00 28.94
ATOM   2599  CD  GLN A 387      25.971   8.286  13.272  1.00 30.39
ATOM   2600  OE1 GLN A 387      27.013   7.619  12.999  1.00 31.54
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ATOM   2601  NE2 GLN A 387      24.782   7.721  13.441  1.00 32.07
ATOM   2602  N   SER A 388      25.186  12.743  14.434  1.00 21.60
ATOM   2603  CA  SER A 388      23.981  13.306  15.055  1.00 21.59
ATOM   2604  C   SER A 388      22.728  12.711  14.429  1.00 22.68
ATOM   2605  O   SER A 388      22.707  12.380  13.203  1.00 23.08
ATOM   2606  CB  SER A 388      23.959  14.824  14.871  1.00 19.88
ATOM   2607  OG  SER A 388      22.661  15.342  15.112  1.00 19.18
ATOM   2608  N   SER A 389      21.681  12.551  15.227  1.00 23.51
ATOM   2609  CA  SER A 389      20.405  12.024  14.690  1.00 24.44
ATOM   2610  C   SER A 389      19.391  13.167  14.708  1.00 23.83
ATOM   2611  O   SER A 389      18.181  12.973  14.385  1.00 23.81
ATOM   2612  CB  SER A 389      19.902  10.847  15.534  1.00 25.63
ATOM   2613  OG  SER A 389      19.681  11.235  16.881  1.00 27.65
ATOM   2614  N   THR A 390      19.861  14.360  15.066  1.00 22.66
ATOM   2615  CA  THR A 390      18.984  15.553  15.127  1.00 22.60
ATOM   2616  C   THR A 390      19.471  16.709  14.260  1.00 21.12
ATOM   2617  O   THR A 390      19.272  17.910  14.608  1.00 21.35
ATOM   2618  CB  THR A 390      18.825  16.052  16.577  1.00 23.02
ATOM   2619  OG1 THR A 390      20.117  16.288  17.150  1.00 24.55
ATOM   2620  CG2 THR A 390      18.079  15.010  17.413  1.00 23.83
ATOM   2621  N   GLY A 391      20.093  16.381  13.136  1.00 19.75
ATOM   2622  CA  GLY A 391      20.573  17.410  12.237  1.00 16.88
ATOM   2623  C   GLY A 391      21.982  17.891  12.526  1.00 17.24
ATOM   2624  O   GLY A 391      22.672  17.402  13.472  1.00 16.27
ATOM   2625  N   THR A 392      22.427  18.851  11.730  1.00 14.99
ATOM   2626  CA  THR A 392      23.773  19.423  11.880  1.00 14.81
ATOM   2627  C   THR A 392      23.841  20.514  12.938  1.00 14.47
ATOM   2628  O   THR A 392      22.949  21.409  13.012  1.00 16.11
ATOM   2629  CB  THR A 392      24.266  20.062  10.564  1.00 12.95
ATOM   2630  OG1 THR A 392      24.494  19.043   9.588  1.00 14.51
ATOM   2631  CG2 THR A 392      25.572  20.839  10.800  1.00 14.09
ATOM   2632  N   VAL A 393      24.857  20.458  13.779  1.00 13.06
ATOM   2633  CA  VAL A 393      25.027  21.534  14.746  1.00 15.07
ATOM   2634  C   VAL A 393      26.462  22.033  14.684  1.00 15.47
ATOM   2635  O   VAL A 393      27.450  21.265  14.908  1.00 16.85
ATOM   2636  CB  VAL A 393      24.619  21.128  16.201  1.00 16.35
ATOM   2637  CG1 VAL A 393      24.559  19.624  16.348  1.00 15.06
ATOM   2638  CG2 VAL A 393      25.566  21.766  17.210  1.00 13.79
ATOM   2639  N   MET A 394      26.592  23.298  14.312  1.00 15.41
ATOM   2640  CA  MET A 394      27.900  23.962  14.231  1.00 16.55
ATOM   2641  C   MET A 394      28.188  24.442  15.647  1.00 16.43
ATOM   2642  O   MET A 394      27.737  25.553  16.059  1.00 14.99
ATOM   2643  CB  MET A 394      27.822  25.143  13.264  1.00 16.88
ATOM   2644  CG  MET A 394      27.607  24.724  11.818  1.00 21.12
ATOM   2645  SD  MET A 394      27.178  26.083  10.700  1.00 27.34
ATOM   2646  CE  MET A 394      25.475  25.768  10.522  1.00 26.22
ATOM   2647  N   GLY A 395      28.909  23.622  16.406  1.00 16.28
ATOM   2648  CA  GLY A 395      29.220  23.967  17.780  1.00 15.87
ATOM   2649  C   GLY A 395      30.487  24.775  17.971  1.00 16.72
ATOM   2650  O   GLY A 395      31.011  25.408  17.005  1.00 16.25
ATOM   2651  N   ALA A 396      30.989  24.769  19.202  1.00 17.29
ATOM   2652  CA  ALA A 396      32.211  25.511  19.586  1.00 19.21
ATOM   2653  C   ALA A 396      33.383  25.310  18.634  1.00 19.63
ATOM   2654  O   ALA A 396      34.050  26.303  18.223  1.00 22.56
ATOM   2655  CB  ALA A 396      32.626  25.128  21.013  1.00 16.95
ATOM   2656  N   VAL A 397      33.661  24.065  18.269  1.00 21.31
ATOM   2657  CA  VAL A 397      34.792  23.781  17.353  1.00 23.40
ATOM   2658  C   VAL A 397      34.690  24.592  16.068  1.00 21.89
ATOM   2659  O   VAL A 397      35.731  25.029  15.496  1.00 24.15
ATOM   2660  CB  VAL A 397      34.874  22.274  17.012  1.00 24.19
ATOM   2661  CG1 VAL A 397      35.065  21.480  18.287  1.00 26.91
ATOM   2662  CG2 VAL A 397      33.623  21.826  16.290  1.00 25.89
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ATOM   2663  N   ILE A 398      33.472  24.805  15.586  1.00 21.78
ATOM   2664  CA  ILE A 398      33.276  25.612  14.359  1.00 21.50
ATOM   2665  C   ILE A 398      33.403  27.086  14.735  1.00 19.91
ATOM   2666  O   ILE A 398      34.222  27.849  14.135  1.00 16.77
ATOM   2667  CB  ILE A 398      31.872  25.390  13.749  1.00 23.48
ATOM   2668  CG1 ILE A 398      31.859  24.113  12.910  1.00 26.70
ATOM   2669  CG2 ILE A 398      31.469  26.596  12.895  1.00 24.67
ATOM   2670  CD1 ILE A 398      32.656  24.223  11.620  1.00 27.64
ATOM   2671  N   MET A 399      32.614  27.492  15.726  1.00 17.64
ATOM   2672  CA  MET A 399      32.594  28.889  16.201  1.00 16.99
ATOM   2673  C   MET A 399      33.951  29.439  16.640  1.00 17.65
ATOM   2674  O   MET A 399      34.202  30.677  16.517  1.00 18.70
ATOM   2675  CB  MET A 399      31.575  29.025  17.331  1.00 15.33
ATOM   2676  CG  MET A 399      30.138  28.800  16.866  1.00 14.30
ATOM   2677  SD  MET A 399      28.891  29.038  18.155  1.00 16.41
ATOM   2678  CE  MET A 399      28.972  30.826  18.388  1.00 10.15
ATOM   2679  N   GLU A 400      34.835  28.579  17.143  1.00 16.09
ATOM   2680  CA  GLU A 400      36.175  29.051  17.580  1.00 16.46
ATOM   2681  C   GLU A 400      36.968  29.576  16.389  1.00 14.50
ATOM   2682  O   GLU A 400      37.971  30.332  16.553  1.00 14.83
ATOM   2683  CB  GLU A 400      36.957  27.919  18.257  1.00 15.95
ATOM   2684  CG  GLU A 400      36.318  27.419  19.540  1.00 18.44
ATOM   2685  CD  GLU A 400      37.156  26.376  20.243  1.00 18.72
ATOM   2686  OE1 GLU A 400      37.771  25.542  19.546  1.00 20.29
ATOM   2687  OE2 GLU A 400      37.186  26.383  21.493  1.00 19.60
ATOM   2688  N   GLY A 401      36.544  29.204  15.190  1.00 13.62
ATOM   2689  CA  GLY A 401      37.246  29.662  14.010  1.00 15.09
ATOM   2690  C   GLY A 401      36.747  31.010  13.533  1.00 16.28
ATOM   2691  O   GLY A 401      37.435  31.693  12.716  1.00 16.14
ATOM   2692  N   PHE A 402      35.591  31.438  14.033  1.00 14.90
ATOM   2693  CA  PHE A 402      35.018  32.712  13.572  1.00 15.01
ATOM   2694  C   PHE A 402      34.378  33.605  14.615  1.00 15.52
ATOM   2695  O   PHE A 402      34.078  33.185  15.777  1.00 16.47
ATOM   2696  CB  PHE A 402      33.966  32.424  12.495  1.00 14.48
ATOM   2697  CG  PHE A 402      34.381  31.364  11.522  1.00 15.64
ATOM   2698  CD1 PHE A 402      34.126  30.021  11.785  1.00 14.91
ATOM   2699  CD2 PHE A 402      35.095  31.700  10.376  1.00 15.20
ATOM   2700  CE1 PHE A 402      34.581  29.027  10.920  1.00 15.18
ATOM   2701  CE2 PHE A 402      35.555  30.717   9.507  1.00 15.72
ATOM   2702  CZ  PHE A 402      35.298  29.376   9.782  1.00 15.12
ATOM   2703  N   TYR A 403      34.168  34.847  14.208  1.00 15.73
ATOM   2704  CA  TYR A 403      33.474  35.837  15.039  1.00 15.81
ATOM   2705  C   TYR A 403      32.071  35.641  14.489  1.00 14.48
ATOM   2706  O   TYR A 403      31.846  35.789  13.250  1.00 15.47
ATOM   2707  CB  TYR A 403      33.977  37.251  14.731  1.00 14.45
ATOM   2708  CG  TYR A 403      33.265  38.340  15.499  1.00 15.22
ATOM   2709  CD1 TYR A 403      32.899  38.152  16.834  1.00 14.85
ATOM   2710  CD2 TYR A 403      33.018  39.584  14.916  1.00 14.28
ATOM   2711  CE1 TYR A 403      32.311  39.175  17.569  1.00 15.25
ATOM   2712  CE2 TYR A 403      32.435  40.617  15.644  1.00 14.12
ATOM   2713  CZ  TYR A 403      32.086  40.406  16.967  1.00 15.72
ATOM   2714  OH  TYR A 403      31.525  41.427  17.697  1.00 18.09
ATOM   2715  N   VAL A 404      31.125  35.286  15.345  1.00 14.70
ATOM   2716  CA  VAL A 404      29.753  35.040  14.854  1.00 14.44
ATOM   2717  C   VAL A 404      28.759  36.079  15.342  1.00 14.92
ATOM   2718  O   VAL A 404      28.552  36.259  16.582  1.00 15.62
ATOM   2719  CB  VAL A 404      29.284  33.629  15.260  1.00 14.39
ATOM   2720  CG1 VAL A 404      27.925  33.323  14.640  1.00 11.90
ATOM   2721  CG2 VAL A 404      30.327  32.603  14.819  1.00 12.73
ATOM   2722  N   VAL A 405      28.136  36.762  14.386  1.00 16.06
ATOM   2723  CA  VAL A 405      27.153  37.822  14.676  1.00 14.31
ATOM   2724  C   VAL A 405      25.717  37.312  14.562  1.00 16.79
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ATOM   2725  O   VAL A 405      25.238  36.955  13.443  1.00 16.14
ATOM   2726  CB  VAL A 405      27.318  39.004  13.700  1.00 13.66
ATOM   2727  CG1 VAL A 405      26.302  40.092  14.021  1.00 12.39
ATOM   2728  CG2 VAL A 405      28.739  39.547  13.775  1.00 10.80
ATOM   2729  N   PHE A 406      25.019  37.260  15.691  1.00 16.73
ATOM   2730  CA  PHE A 406      23.616  36.805  15.685  1.00 16.71
ATOM   2731  C   PHE A 406      22.755  38.049  15.531  1.00 17.47
ATOM   2732  O   PHE A 406      22.286  38.654  16.539  1.00 17.39
ATOM   2733  CB  PHE A 406      23.287  36.053  16.979  1.00 13.96
ATOM   2734  CG  PHE A 406      24.061  34.765  17.139  1.00 13.82
ATOM   2735  CD1 PHE A 406      25.398  34.783  17.533  1.00 13.31
ATOM   2736  CD2 PHE A 406      23.464  33.538  16.863  1.00 12.85
ATOM   2737  CE1 PHE A 406      26.128  33.601  17.646  1.00 13.23
ATOM   2738  CE2 PHE A 406      24.185  32.350  16.973  1.00 12.78
ATOM   2739  CZ  PHE A 406      25.522  32.382  17.367  1.00 12.96
ATOM   2740  N   ASP A 407      22.566  38.449  14.278  1.00 18.08
ATOM   2741  CA  ASP A 407      21.785  39.647  13.932  1.00 19.70
ATOM   2742  C   ASP A 407      20.297  39.316  13.927  1.00 19.73
ATOM   2743  O   ASP A 407      19.675  39.120  12.837  1.00 18.96
ATOM   2744  CB  ASP A 407      22.221  40.153  12.552  1.00 22.61
ATOM   2745  CG  ASP A 407      21.663  41.530  12.223  1.00 24.28
ATOM   2746  OD1 ASP A 407      20.660  41.935  12.849  1.00 24.12
ATOM   2747  OD2 ASP A 407      22.225  42.198  11.325  1.00 23.37
ATOM   2748  N   ARG A 408      19.709  39.245  15.116  1.00 19.72
ATOM   2749  CA  ARG A 408      18.269  38.928  15.259  1.00 22.01
ATOM   2750  C   ARG A 408      17.393  39.967  14.557  1.00 21.56
ATOM   2751  O   ARG A 408      16.386  39.606  13.875  1.00 20.49
ATOM   2752  CB  ARG A 408      17.909  38.835  16.748  1.00 23.44
ATOM   2753  CG  ARG A 408      18.670  37.724  17.479  1.00 25.61
ATOM   2754  CD  ARG A 408      18.838  37.994  18.973  1.00 28.14
ATOM   2755  NE  ARG A 408      17.843  37.328  19.814  1.00 31.17
ATOM   2756  CZ  ARG A 408      16.567  37.679  19.887  1.00 32.24
ATOM   2757  NH1 ARG A 408      16.127  38.693  19.163  1.00 35.70
ATOM   2758  NH2 ARG A 408      15.735  37.029  20.687  1.00 31.13
ATOM   2759  N   ALA A 409      17.750  41.241  14.694  1.00 21.10
ATOM   2760  CA  ALA A 409      16.978  42.329  14.056  1.00 22.43
ATOM   2761  C   ALA A 409      16.785  42.050  12.571  1.00 22.80
ATOM   2762  O   ALA A 409      15.646  42.177  12.034  1.00 24.04
ATOM   2763  CB  ALA A 409      17.689  43.664  14.247  1.00 20.85
ATOM   2764  N   ARG A 410      17.858  41.664  11.889  1.00 23.89
ATOM   2765  CA  ARG A 410      17.770  41.374  10.445  1.00 25.07
ATOM   2766  C   ARG A 410      17.639  39.888  10.119  1.00 24.26
ATOM   2767  O   ARG A 410      17.908  39.461   8.956  1.00 24.63
ATOM   2768  CB  ARG A 410      18.987  41.949   9.724  1.00 26.83
ATOM   2769  CG  ARG A 410      19.025  43.464   9.700  1.00 29.89
ATOM   2770  CD  ARG A 410      19.326  43.944   8.295  1.00 32.69
ATOM   2771  NE  ARG A 410      20.590  44.664   8.208  1.00 33.51
ATOM   2772  CZ  ARG A 410      21.182  44.979   7.062  1.00 34.58
ATOM   2773  NH1 ARG A 410      20.626  44.631   5.907  1.00 33.99
ATOM   2774  NH2 ARG A 410      22.328  45.644   7.068  1.00 35.27
ATOM   2775  N   LYS A 411      17.223  39.091  11.097  1.00 22.77
ATOM   2776  CA  LYS A 411      17.061  37.630  10.891  1.00 22.97
ATOM   2777  C   LYS A 411      18.227  37.031  10.104  1.00 21.80
ATOM   2778  O   LYS A 411      18.015  36.309   9.081  1.00 20.39
ATOM   2779  CB  LYS A 411      15.761  37.335  10.138  1.00 23.53
ATOM   2780  CG  LYS A 411      14.491  37.686  10.886  1.00 27.80
ATOM   2781  CD  LYS A 411      13.270  37.188  10.121  1.00 30.25
ATOM   2782  CE  LYS A 411      13.337  35.678   9.890  1.00 31.18
ATOM   2783  NZ  LYS A 411      12.153  35.163   9.142  1.00 34.08
ATOM   2784  N   ARG A 412      19.449  37.290  10.541  1.00 19.85
ATOM   2785  CA  ARG A 412      20.607  36.748   9.815  1.00 18.29
ATOM   2786  C   ARG A 412      21.789  36.505  10.736  1.00 18.54
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ATOM   2787  O   ARG A 412      21.911  37.137  11.837  1.00 18.56
ATOM   2788  CB  ARG A 412      21.019  37.714   8.703  1.00 18.72
ATOM   2789  CG  ARG A 412      21.571  39.027   9.239  1.00 18.66
ATOM   2790  CD  ARG A 412      21.941  39.988   8.127  1.00 18.34
ATOM   2791  NE  ARG A 412      22.560  41.196   8.662  1.00 19.28
ATOM   2792  CZ  ARG A 412      23.082  42.163   7.916  1.00 20.03
ATOM   2793  NH1 ARG A 412      23.059  42.067   6.591  1.00 19.36
ATOM   2794  NH2 ARG A 412      23.635  43.219   8.496  1.00 19.27
ATOM   2795  N   ILE A 413      22.668  35.606  10.317  1.00 17.01
ATOM   2796  CA  ILE A 413      23.865  35.285  11.103  1.00 16.43
ATOM   2797  C   ILE A 413      25.103  35.576  10.266  1.00 16.20
ATOM   2798  O   ILE A 413      25.213  35.125   9.084  1.00 17.17
ATOM   2799  CB  ILE A 413      23.855  33.808  11.533  1.00 16.02
ATOM   2800  CG1 ILE A 413      22.667  33.562  12.469  1.00 13.92
ATOM   2801  CG2 ILE A 413      25.168  33.458  12.218  1.00 15.95
ATOM   2802  CD1 ILE A 413      22.482  32.130  12.862  1.00 14.89
ATOM   2803  N   GLY A 414      26.028  36.332  10.841  1.00 15.43
ATOM   2804  CA  GLY A 414      27.243  36.679  10.132  1.00 14.42
ATOM   2805  C   GLY A 414      28.463  35.899  10.585  1.00 14.91
ATOM   2806  O   GLY A 414      28.569  35.463  11.779  1.00 12.74
ATOM   2807  N   PHE A 415      29.392  35.709   9.656  1.00 12.70
ATOM   2808  CA  PHE A 415      30.638  34.977   9.932  1.00 14.84
ATOM   2809  C   PHE A 415      31.823  35.766   9.403  1.00 15.05
ATOM   2810  O   PHE A 415      31.761  36.376   8.291  1.00 17.34
ATOM   2811  CB  PHE A 415      30.613  33.599   9.256  1.00 13.57
ATOM   2812  CG  PHE A 415      29.628  32.640   9.860  1.00 13.35
ATOM   2813  CD1 PHE A 415      30.034  31.710  10.820  1.00 14.56
ATOM   2814  CD2 PHE A 415      28.296  32.660   9.472  1.00 11.54
ATOM   2815  CE1 PHE A 415      29.117  30.809  11.383  1.00 13.74
ATOM   2816  CE2 PHE A 415      27.373  31.768  10.027  1.00 12.67
ATOM   2817  CZ  PHE A 415      27.787  30.839  10.985  1.00 13.15
ATOM   2818  N   ALA A 416      32.895  35.779  10.178  1.00 15.11
ATOM   2819  CA  ALA A 416      34.135  36.470   9.786  1.00 14.57
ATOM   2820  C   ALA A 416      35.248  35.738  10.515  1.00 14.48
ATOM   2821  O   ALA A 416      35.027  35.186  11.639  1.00 12.56
ATOM   2822  CB  ALA A 416      34.095  37.935  10.208  1.00 11.46
ATOM   2823  N   VAL A 417      36.425  35.692   9.906  1.00 14.71
ATOM   2824  CA  VAL A 417      37.569  35.011  10.528  1.00 16.80
ATOM   2825  C   VAL A 417      37.835  35.634  11.892  1.00 18.08
ATOM   2826  O   VAL A 417      37.922  36.901  12.033  1.00 17.13
ATOM   2827  CB  VAL A 417      38.824  35.126   9.642  1.00 17.67
ATOM   2828  CG1 VAL A 417      40.022  34.486  10.333  1.00 16.83
ATOM   2829  CG2 VAL A 417      38.561  34.441   8.301  1.00 18.32
ATOM   2830  N   SER A 418      37.953  34.785  12.905  1.00 17.31
ATOM   2831  CA  SER A 418      38.201  35.271  14.272  1.00 17.62
ATOM   2832  C   SER A 418      39.637  35.712  14.455  1.00 18.36
ATOM   2833  O   SER A 418      40.591  35.038  13.963  1.00 19.44
ATOM   2834  CB  SER A 418      37.882  34.182  15.295  1.00 18.09
ATOM   2835  OG  SER A 418      38.228  34.617  16.599  1.00 17.42
ATOM   2836  N   ALA A 419      39.821  36.827  15.150  1.00 17.60
ATOM   2837  CA  ALA A 419      41.175  37.335  15.410  1.00 18.46
ATOM   2838  C   ALA A 419      41.877  36.423  16.423  1.00 19.09
ATOM   2839  O   ALA A 419      43.117  36.553  16.649  1.00 19.60
ATOM   2840  CB  ALA A 419      41.106  38.772  15.943  1.00 17.70
ATOM   2841  N   CYS A 420      41.132  35.500  17.032  1.00 19.36
ATOM   2842  CA  CYS A 420      41.736  34.575  18.029  1.00 20.89
ATOM   2843  C   CYS A 420      41.677  33.105  17.624  1.00 19.60
ATOM   2844  O   CYS A 420      41.805  32.202  18.501  1.00 22.74
ATOM   2845  CB  CYS A 420      41.064  34.734  19.410  1.00 21.69
ATOM   2846  SG  CYS A 420      39.353  34.096  19.526  1.00 25.02
ATOM   2847  N   HIS A 421      41.495  32.814  16.342  1.00 17.86
ATOM   2848  CA  HIS A 421      41.435  31.393  15.933  1.00 17.71
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ATOM   2849  C   HIS A 421      42.834  30.798  15.799  1.00 17.18
ATOM   2850  O   HIS A 421      43.801  31.495  15.356  1.00 14.17
ATOM   2851  CB  HIS A 421      40.641  31.236  14.625  1.00 18.65
ATOM   2852  CG  HIS A 421      41.433  31.504  13.381  1.00 18.77
ATOM   2853  ND1 HIS A 421      42.114  30.514  12.705  1.00 18.84
ATOM   2854  CD2 HIS A 421      41.631  32.645  12.678  1.00 18.73
ATOM   2855  CE1 HIS A 421      42.695  31.032  11.637  1.00 17.98
ATOM   2856  NE2 HIS A 421      42.418  32.323  11.597  1.00 20.03
ATOM   2857  N   VAL A 422      42.965  29.533  16.194  1.00 16.96
ATOM   2858  CA  VAL A 422      44.260  28.816  16.132  1.00 16.89
ATOM   2859  C   VAL A 422      44.571  28.334  14.719  1.00 17.53
ATOM   2860  O   VAL A 422      43.678  27.764  14.021  1.00 17.13
ATOM   2861  CB  VAL A 422      44.257  27.588  17.061  1.00 16.92
ATOM   2862  CG1 VAL A 422      45.632  26.938  17.063  1.00 15.15
ATOM   2863  CG2 VAL A 422      43.850  28.004  18.479  1.00 19.33
ATOM   2864  N   HIS A 423      45.815  28.531  14.291  1.00 16.64
ATOM   2865  CA  HIS A 423      46.264  28.112  12.940  1.00 16.92
ATOM   2866  C   HIS A 423      47.792  28.038  12.906  1.00 17.46
ATOM   2867  O   HIS A 423      48.461  28.105  13.981  1.00 17.20
ATOM   2868  CB  HIS A 423      45.755  29.111  11.889  1.00 15.85
ATOM   2869  CG  HIS A 423      46.242  30.512  12.096  1.00 18.62
ATOM   2870  ND1 HIS A 423      47.390  30.998  11.504  1.00 19.80
ATOM   2871  CD2 HIS A 423      45.758  31.522  12.857  1.00 17.42
ATOM   2872  CE1 HIS A 423      47.590  32.245  11.892  1.00 18.22
ATOM   2873  NE2 HIS A 423      46.615  32.586  12.714  1.00 18.53
ATOM   2874  N   ASP A 424      48.360  27.869  11.714  1.00 18.00
ATOM   2875  CA  ASP A 424      49.836  27.817  11.556  1.00 17.75
ATOM   2876  C   ASP A 424      50.194  28.804  10.453  1.00 18.36
ATOM   2877  O   ASP A 424      49.294  29.527   9.935  1.00 20.02
ATOM   2878  CB  ASP A 424      50.305  26.396  11.206  1.00 18.00
ATOM   2879  CG  ASP A 424      49.545  25.791  10.037  1.00 19.08
ATOM   2880  OD1 ASP A 424      49.110  24.623  10.149  1.00 18.99
ATOM   2881  OD2 ASP A 424      49.390  26.473   9.003  1.00 20.46
ATOM   2882  N   GLU A 425      51.459  28.877  10.063  1.00 17.55
ATOM   2883  CA  GLU A 425      51.813  29.853   9.015  1.00 18.77
ATOM   2884  C   GLU A 425      51.497  29.379   7.601  1.00 16.95
ATOM   2885  O   GLU A 425      51.724  30.131   6.613  1.00 17.24
ATOM   2886  CB  GLU A 425      53.289  30.239   9.112  1.00 18.65
ATOM   2887  CG  GLU A 425      54.254  29.150   8.714  1.00 20.84
ATOM   2888  CD  GLU A 425      55.632  29.697   8.381  1.00 21.89
ATOM   2889  OE1 GLU A 425      56.481  28.901   7.936  1.00 22.61
ATOM   2890  OE2 GLU A 425      55.867  30.920   8.559  1.00 22.65
ATOM   2891  N   PHE A 426      50.955  28.171   7.476  1.00 14.60
ATOM   2892  CA  PHE A 426      50.619  27.606   6.150  1.00 13.51
ATOM   2893  C   PHE A 426      49.157  27.767   5.763  1.00 15.14
ATOM   2894  O   PHE A 426      48.826  27.822   4.540  1.00 16.10
ATOM   2895  CB  PHE A 426      51.001  26.127   6.109  1.00 14.53
ATOM   2896  CG  PHE A 426      52.452  25.877   6.400  1.00 14.20
ATOM   2897  CD1 PHE A 426      53.433  26.244   5.482  1.00 13.59
ATOM   2898  CD2 PHE A 426      52.841  25.298   7.606  1.00 14.11
ATOM   2899  CE1 PHE A 426      54.787  26.040   5.762  1.00 14.83
ATOM   2900  CE2 PHE A 426      54.192  25.087   7.897  1.00 15.49
ATOM   2901  CZ  PHE A 426      55.167  25.460   6.969  1.00 14.08
ATOM   2902  N   ARG A 427      48.269  27.827   6.752  1.00 13.77
ATOM   2903  CA  ARG A 427      46.824  27.985   6.469  1.00 14.89
ATOM   2904  C   ARG A 427      46.130  28.695   7.615  1.00 15.43
ATOM   2905  O   ARG A 427      46.630  28.710   8.781  1.00 14.58
ATOM   2906  CB  ARG A 427      46.132  26.632   6.301  1.00 15.33
ATOM   2907  CG  ARG A 427      46.959  25.518   5.707  1.00 16.84
ATOM   2908  CD  ARG A 427      46.645  24.234   6.477  1.00 17.68
ATOM   2909  NE  ARG A 427      45.994  23.230   5.655  1.00 16.69
ATOM   2910  CZ  ARG A 427      45.701  21.998   6.062  1.00 15.45
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ATOM	2911	NH1	ARG	A	427	45.114	21.159	5.224	1.00	14.20
ATOM	2912	NH2	ARG	A	427	45.981	21.603	7.296	1.00	13.31
ATOM	2913	N	THR	A	428	44.976	29.269	7.317	1.00	15.28
ATOM	2914	CA	THR	A	428	44.180	29.967	8.336	1.00	17.94
ATOM	2915	C	THR	A	428	42.731	29.650	8.041	1.00	16.25
ATOM	2916	O	THR	A	428	42.400	29.165	6.923	1.00	14.77
ATOM	2917	CB	THR	A	428	44.353	31.503	8.249	1.00	18.18
ATOM	2918	OG1	THR	A	428	44.043	31.942	6.921	1.00	20.24
ATOM	2919	CG2	THR	A	428	45.773	31.901	8.583	1.00	19.84
ATOM	2920	N	ALA	A	429	41.860	29.901	9.009	1.00	16.14
ATOM	2921	CA	ALA	A	429	40.423	29.677	8.803	1.00	16.03
ATOM	2922	C	ALA	A	429	40.048	30.739	7.775	1.00	15.66
ATOM	2923	O	ALA	A	429	40.808	31.738	7.574	1.00	14.51
ATOM	2924	CB	ALA	A	429	39.656	29.898	10.105	1.00	17.08
ATOM	2925	N	ALA	A	430	38.920	30.575	7.107	1.00	14.04
ATOM	2926	CA	ALA	A	430	38.556	31.576	6.100	1.00	13.71
ATOM	2927	C	ALA	A	430	37.067	31.706	5.883	1.00	11.98
ATOM	2928	O	ALA	A	430	36.271	30.754	6.166	1.00	12.33
ATOM	2929	CB	ALA	A	430	39.251	31.246	4.762	1.00	12.27
ATOM	2930	N	VAL	A	431	36.671	32.874	5.396	1.00	11.01
ATOM	2931	CA	VAL	A	431	35.260	33.149	5.076	1.00	13.39
ATOM	2932	C	VAL	A	431	35.344	33.773	3.697	1.00	15.69
ATOM	2933	O	VAL	A	431	35.857	34.926	3.533	1.00	17.86
ATOM	2934	CB	VAL	A	431	34.624	34.145	6.056	1.00	11.50
ATOM	2935	CG1	VAL	A	431	33.148	34.294	5.737	1.00	10.61
ATOM	2936	CG2	VAL	A	431	34.818	33.659	7.494	1.00	10.71
ATOM	2937	N	GLU	A	432	34.874	33.048	2.694	1.00	16.74
ATOM	2938	CA	GLU	A	432	34.969	33.544	1.320	1.00	18.65
ATOM	2939	C	GLU	A	432	33.681	33.414	0.530	1.00	18.40
ATOM	2940	O	GLU	A	432	32.794	32.567	0.852	1.00	16.81
ATOM	2941	CB	GLU	A	432	36.097	32.796	0.607	1.00	19.91
ATOM	2942	CG	GLU	A	432	37.460	33.031	1.241	1.00	24.66
ATOM	2943	CD	GLU	A	432	38.466	31.930	0.935	1.00	27.80
ATOM	2944	OE1	GLU	A	432	39.681	32.196	1.051	1.00	30.84
ATOM	2945	OE2	GLU	A	432	38.049	30.799	0.595	1.00	28.87
ATOM	2946	N	GLY	A	433	33.574	34.243	-0.504	1.00	18.95
ATOM	2947	CA	GLY	A	433	32.408	34.244	-1.363	1.00	19.36
ATOM	2948	C	GLY	A	433	32.504	35.385	-2.359	1.00	19.59
ATOM	2949	O	GLY	A	433	33.489	36.173	-2.328	1.00	18.33
ATOM	2950	N	PRO	A	434	31.511	35.539	-3.243	1.00	19.47
ATOM	2951	CA	PRO	A	434	30.345	34.655	-3.285	1.00	19.72
ATOM	2952	C	PRO	A	434	30.485	33.589	-4.353	1.00	19.98
ATOM	2953	O	PRO	A	434	31.382	33.674	-5.235	1.00	22.24
ATOM	2954	CB	PRO	A	434	29.215	35.619	-3.595	1.00	19.80
ATOM	2955	CG	PRO	A	434	29.869	36.517	-4.616	1.00	19.70
ATOM	2956	CD	PRO	A	434	31.261	36.770	-4.018	1.00	19.73
ATOM	2957	N	PHE	A	435	29.624	32.583	-4.290	1.00	21.45
ATOM	2958	CA	PHE	A	435	29.619	31.502	-5.292	1.00	22.31
ATOM	2959	C	PHE	A	435	28.217	31.513	-5.872	1.00	24.39
ATOM	2960	O	PHE	A	435	27.207	31.636	-5.110	1.00	24.58
ATOM	2961	CB	PHE	A	435	29.924	30.155	-4.636	1.00	22.02
ATOM	2962	CG	PHE	A	435	31.215	30.141	-3.876	1.00	20.80
ATOM	2963	CD1	PHE	A	435	31.232	30.392	-2.507	1.00	20.70
ATOM	2964	CD2	PHE	A	435	32.424	29.945	-4.542	1.00	21.70
ATOM	2965	CE1	PHE	A	435	32.432	30.451	-1.809	1.00	20.27
ATOM	2966	CE2	PHE	A	435	33.634	30.003	-3.853	1.00	21.68
ATOM	2967	CZ	PHE	A	435	33.637	30.259	-2.481	1.00	21.51
ATOM	2968	N	VAL	A	436	28.117	31.396	-7.192	1.00	27.02
ATOM	2969	CA	VAL	A	436	26.802	31.438	-7.872	1.00	29.79
ATOM	2970	C	VAL	A	436	26.526	30.219	-8.739	1.00	32.85
ATOM	2971	O	VAL	A	436	25.434	30.120	-9.376	1.00	33.81
ATOM	2972	CB	VAL	A	436	26.702	32.677	-8.787	1.00	28.98

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ATOM   2973  CG1 VAL A 436      26.999  33.944  -7.996  1.00 29.00
ATOM   2974  CG2 VAL A 436      27.678  32.537  -9.947  1.00 28.49
ATOM   2975  N   THR A 437      27.473  29.292  -8.795  1.00 36.05
ATOM   2976  CA  THR A 437      27.305  28.089  -9.638  1.00 39.30
ATOM   2977  C   THR A 437      26.582  26.979  -8.870  1.00 41.99
ATOM   2978  O   THR A 437      26.604  25.775  -9.276  1.00 41.77
ATOM   2979  CB  THR A 437      28.690  27.592 -10.123  1.00 39.02
ATOM   2980  OG1 THR A 437      28.552  26.981 -11.408  1.00 42.51
ATOM   2981  CG2 THR A 437      29.280  26.578  -9.156  1.00 38.10
ATOM   2982  N   LEU A 438      25.908  27.368  -7.794  1.00 45.33
ATOM   2983  CA  LEU A 438      25.199  26.417  -6.901  1.00 49.22
ATOM   2984  C   LEU A 438      23.753  26.016  -7.165  1.00 50.49
ATOM   2985  O   LEU A 438      22.869  26.878  -7.466  1.00 51.99
ATOM   2986  CB  LEU A 438      25.276  26.944  -5.473  1.00 50.30
ATOM   2987  CG  LEU A 438      26.027  28.269  -5.358  1.00 50.73
ATOM   2988  CD1 LEU A 438      25.108  29.457  -5.584  1.00 50.27
ATOM   2989  CD2 LEU A 438      26.629  28.328  -4.001  1.00 51.67
ATOM   2990  N   ASP A 439      23.505  24.715  -7.037  1.00 52.67
ATOM   2991  CA  ASP A 439      22.149  24.128  -7.172  1.00 55.74
ATOM   2992  C   ASP A 439      21.690  24.224  -5.722  1.00 56.96
ATOM   2993  O   ASP A 439      21.757  23.221  -4.945  1.00 57.33
ATOM   2994  CB  ASP A 439      22.240  22.657  -7.586  1.00 56.39
ATOM   2995  CG  ASP A 439      20.879  21.993  -7.695  1.00 57.68
ATOM   2996  OD1 ASP A 439      20.046  22.178  -6.781  1.00 57.75
ATOM   2997  OD2 ASP A 439      20.645  21.274  -8.692  1.00 58.18
ATOM   2998  N   MET A 440      21.233  25.407  -5.337  1.00 58.71
ATOM   2999  CA  MET A 440      20.841  25.656  -3.944  1.00 60.87
ATOM   3000  C   MET A 440      19.435  26.215  -3.713  1.00 62.52
ATOM   3001  O   MET A 440      19.247  27.451  -3.489  1.00 63.93
ATOM   3002  CB  MET A 440      21.916  26.569  -3.346  1.00 60.48
ATOM   3003  CG  MET A 440      21.523  27.456  -2.201  1.00 60.72
ATOM   3004  SD  MET A 440      22.755  28.755  -2.086  1.00 59.28
ATOM   3005  CE  MET A 440      22.367  29.689  -3.543  1.00 59.46
ATOM   3006  N   GLU A 441      18.435  25.343  -3.765  1.00 63.61
ATOM   3007  CA  GLU A 441      17.042  25.774  -3.514  1.00 65.54
ATOM   3008  C   GLU A 441      16.356  24.847  -2.518  1.00 64.49
ATOM   3009  O   GLU A 441      15.998  25.285  -1.375  1.00 65.36
ATOM   3010  CB  GLU A 441      16.229  25.847  -4.815  1.00 67.99
ATOM   3011  CG  GLU A 441      16.500  24.745  -5.822  1.00 70.98
ATOM   3012  CD  GLU A 441      17.353  25.228  -6.981  1.00 72.23
ATOM   3013  OE1 GLU A 441      18.507  25.646  -6.742  1.00 73.24
ATOM   3014  OE2 GLU A 441      16.867  25.194  -8.132  1.00 73.30
ATOM   3015  N   ASP A 442      16.170  23.585  -2.896  1.00 61.29
ATOM   3016  CA  ASP A 442      15.519  22.616  -1.986  1.00 58.37
ATOM   3017  C   ASP A 442      16.504  21.966  -1.018  1.00 55.47
ATOM   3018  O   ASP A 442      16.615  20.704  -0.950  1.00 54.59
ATOM   3019  CB  ASP A 442      14.800  21.530  -2.785  1.00 59.93
ATOM   3020  CG  ASP A 442      13.298  21.616  -2.646  1.00 60.90
ATOM   3021  OD1 ASP A 442      12.689  22.478  -3.312  1.00 61.34
ATOM   3022  OD2 ASP A 442      12.729  20.832  -1.854  1.00 61.81
ATOM   3023  N   CYS A 443      17.207  22.790  -0.252  1.00 51.31
ATOM   3024  CA  CYS A 443      18.200  22.281   0.713  1.00 47.79
ATOM   3025  C   CYS A 443      17.635  22.156   2.121  1.00 46.40
ATOM   3026  O   CYS A 443      18.168  21.373   2.965  1.00 44.04
ATOM   3027  CB  CYS A 443      19.421  23.198   0.713  1.00 48.61
ATOM   3028  SG  CYS A 443      20.176  23.339  -0.939  1.00 46.95
ATOM   3029  N   GLY A 444      16.566  22.895   2.395  1.00 45.40
ATOM   3030  CA  GLY A 444      15.953  22.846   3.709  1.00 45.06
ATOM   3031  C   GLY A 444      15.011  21.673   3.899  1.00 45.25
ATOM   3032  O   GLY A 444      14.271  21.264   2.952  1.00 44.97
ATOM   3033  N   TYR A 445      15.018  21.109   5.101  1.00 44.97
ATOM   3034  CA  TYR A 445      14.140  19.968   5.421  1.00 44.48
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ATOM   3035  C   TYR A 445      12.778  20.467   5.882  1.00 45.23
ATOM   3036  O   TYR A 445      12.662  21.558   6.530  1.00 44.57
ATOM   3037  CB  TYR A 445      14.801  19.172   6.531  1.00 43.11
ATOM   3038  CG  TYR A 445      13.918  17.997   6.871  1.00 42.75
ATOM   3039  CD1 TYR A 445      13.846  16.905   6.010  1.00 42.58
ATOM   3040  CD2 TYR A 445      13.170  17.998   8.049  1.00 42.27
ATOM   3041  CE1 TYR A 445      13.042  15.820   6.327  1.00 41.99
ATOM   3042  CE2 TYR A 445      12.358  16.917   8.360  1.00 43.20
ATOM   3043  CZ  TYR A 445      12.289  15.835   7.503  1.00 41.98
ATOM   3044  OH  TYR A 445      11.490  14.751   7.810  1.00 20.00
ATOM   3045  N   ASN A 446      11.746  19.699   5.550  1.00 45.69
ATOM   3046  CA  ASN A 446      10.359  20.012   5.947  1.00 48.64
ATOM   3047  C   ASN A 446       9.776  18.726   6.524  1.00 50.90
ATOM   3048  O   ASN A 446       9.894  17.625   5.896  1.00 51.59
ATOM   3049  CB  ASN A 446       9.537  20.470   4.738  1.00 48.19
ATOM   3050  CG  ASN A 446       9.975  21.827   4.213  1.00 48.18
ATOM   3051  OD1 ASN A 446       9.926  22.858   4.950  1.00 48.63
ATOM   3052  ND2 ASN A 446      10.403  21.867   2.957  1.00 48.04
ATOM   3053  N   ILE A 447       9.165  18.826   7.700  1.00 53.94
ATOM   3054  CA  ILE A 447       8.569  17.650   8.388  1.00 55.99
ATOM   3055  C   ILE A 447       7.720  16.772   7.463  1.00 57.01
ATOM   3056  O   ILE A 447       7.449  17.195   6.318  1.00 58.11
ATOM   3057  CB  ILE A 447       7.699  18.105   9.577  1.00 55.86
ATOM   3058  CG1 ILE A 447       8.488  19.086  10.450  1.00 56.28
ATOM   3059  CG2 ILE A 447       7.267  16.900  10.406  1.00 56.92
ATOM   3060  CD1 ILE A 447       9.759  18.505  11.037  1.00 55.79
ATOM   3061  OXT ILE A 447       7.328  15.666   7.895  1.00 57.55
ATOM   3062  N   SER P   1      35.528  15.672  28.238  1.00 37.61
ATOM   3063  CA  SER P   1      34.172  16.082  28.590  1.00 36.72
ATOM   3064  C   SER P   1      33.508  16.863  27.450  1.00 34.75
ATOM   3065  O   SER P   1      34.132  17.643  26.742  1.00 36.46
ATOM   3066  CB  SER P   1      34.248  16.949  29.848  1.00 37.77
ATOM   3067  OG  SER P   1      33.152  17.865  29.853  1.00 40.82
ATOM   3068  N   GLU P   2      32.203  16.601  27.257  1.00 32.86
ATOM   3069  CA  GLU P   2      31.513  17.216  26.129  1.00 32.80
ATOM   3070  C   GLU P   2      30.218  17.906  26.552  1.00 31.23
ATOM   3071  O   GLU P   2      29.435  17.401  27.348  1.00 31.31
ATOM   3072  CB  GLU P   2      31.275  16.167  25.027  1.00 33.64
ATOM   3073  CG  GLU P   2      31.096  17.096  23.826  1.00 37.41
ATOM   3074  CD  GLU P   2      31.076  15.940  22.852  1.00 38.37
ATOM   3075  OE1 GLU P   2      31.996  15.134  22.983  1.00 39.04
ATOM   3076  OE2 GLU P   2      30.175  15.798  22.037  1.00 39.43
ATOM   3077  N   VAL P   3      29.742  19.344  26.106  1.00 27.98
ATOM   3078  CA  VAL P   3      28.367  19.820  26.101  1.00 26.44
ATOM   3079  C   VAL P   3      27.717  19.598  24.735  1.00 26.26
ATOM   3080  O   VAL P   3      28.371  19.580  23.701  1.00 25.48
ATOM   3081  CB  VAL P   3      28.377  21.311  26.429  1.00 25.89
ATOM   3082  CG1 VAL P   3      28.684  21.516  27.911  1.00 27.07
ATOM   3083  CG2 VAL P   3      29.431  22.012  25.594  1.00 23.97
ATOM   3084  N   ASN P   4      26.361  19.591  25.174  1.00 25.89
ATOM   3085  CA  ASN P   4      25.421  19.254  24.075  1.00 26.64
ATOM   3086  C   ASN P   4      24.027  19.825  24.452  1.00 26.87
ATOM   3087  O   ASN P   4      23.116  19.163  25.077  1.00 27.10
ATOM   3088  CB  ASN P   4      25.349  17.766  23.876  1.00 27.95
ATOM   3089  CG  ASN P   4      26.498  17.245  22.971  1.00 29.39
ATOM   3090  OD1 ASN P   4      26.499  17.409  21.723  1.00 31.90
ATOM   3091  ND2 ASN P   4      27.489  16.617  23.603  1.00 31.97
ATOM   3092  N   STA P   5      24.115  21.101  24.323  1.00 25.26
ATOM   3093  CA  STA P   5      22.965  21.865  24.929  1.00 25.83
ATOM   3094  CB  STA P   5      23.683  22.681  26.021  1.00 27.28
ATOM   3095  CG  STA P   5      24.378  22.057  27.197  1.00 28.07
ATOM   3096  CD1 STA P   5      25.002  23.077  28.182  1.00 27.46
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ATOM   3097  CD2 STA P   5      23.280  21.130  27.828  1.00 25.47
ATOM   3098  CH  STA P   5      22.223  22.851  23.940  1.00 25.86
ATOM   3099  OH  STA P   5      23.028  23.679  23.298  1.00 25.23
ATOM   3100  CM  STA P   5      21.372  21.980  23.048  1.00 27.11
ATOM   3101  C   STA P   5      20.420  21.340  24.125  1.00 27.81
ATOM   3102  O   STA P   5      20.241  20.065  24.095  1.00 25.70
ATOM   3103  N   VAL P   6      19.339  22.479  23.764  1.00 26.04
ATOM   3104  CA  VAL P   6      18.037  21.953  24.156  1.00 27.12
ATOM   3105  C   VAL P   6      17.496  20.965  23.121  1.00 27.36
ATOM   3106  O   VAL P   6      17.795  21.029  21.936  1.00 26.97
ATOM   3107  CB  VAL P   6      17.073  23.130  24.312  1.00 27.18
ATOM   3108  CG1 VAL P   6      16.433  23.463  22.965  1.00 26.70
ATOM   3109  CG2 VAL P   6      15.985  22.781  25.311  1.00 28.74
ATOM   3110  N   ALA P   7      16.702  19.998  23.617  1.00 28.68
ATOM   3111  CA  ALA P   7      16.158  18.986  22.720  1.00 32.14
ATOM   3112  C   ALA P   7      14.774  19.377  22.197  1.00 32.99
ATOM   3113  O   ALA P   7      14.040  20.149  22.801  1.00 32.08
ATOM   3114  CB  ALA P   7      16.072  17.666  23.489  1.00 31.38
ATOM   3115  N   GLU P   8      14.443  18.843  21.007  1.00 36.10
ATOM   3116  CA  GLU P   8      13.144  19.143  20.418  1.00 39.90
ATOM   3117  C   GLU P   8      12.012  18.425  21.158  1.00 41.72
ATOM   3118  O   GLU P   8      12.189  17.359  21.733  1.00 41.52
ATOM   3119  CB  GLU P   8      13.172  18.705  18.952  1.00 39.88
ATOM   3120  CG  GLU P   8      14.037  19.626  18.090  1.00 41.02
ATOM   3121  CD  GLU P   8      13.896  19.235  16.637  1.00 41.83
ATOM   3122  OE1 GLU P   8      14.911  19.052  15.979  1.00 41.60
ATOM   3123  OE2 GLU P   8      12.765  19.124  16.169  1.00 41.88
ATOM   3124  N   PHE P   9      10.811  18.986  21.162  1.00 45.62
ATOM   3125  CA  PHE P   9       9.677  18.356  21.865  1.00 49.63
ATOM   3126  C   PHE P   9       9.382  16.960  21.337  1.00 50.61
ATOM   3127  O   PHE P   9       9.156  16.839  20.116  1.00 51.38
ATOM   3128  CB  PHE P   9       8.451  19.245  21.670  1.00 50.65
ATOM   3129  CG  PHE P   9       8.607  20.501  22.499  1.00 52.48
ATOM   3130  CD1 PHE P   9       8.278  20.493  23.849  1.00 52.80
ATOM   3131  CD2 PHE P   9       9.073  21.659  21.899  1.00 53.12
ATOM   3132  CE1 PHE P   9       8.420  21.651  24.600  1.00 53.74
ATOM   3133  CE2 PHE P   9       9.215  22.817  22.659  1.00 53.61
ATOM   3134  CZ  PHE P   9       8.890  22.817  24.010  1.00 54.24
ATOM   3135  OXT PHE P   9       9.383  16.011  22.152  1.00 51.56
ATOM   3136  OH2 TIP C   2      37.673   4.149  14.933  1.00 18.73
ATOM   3137  OH2 TIP C   3      37.999  19.019  28.545  1.00 20.36
ATOM   3138  OH2 TIP C  12      46.550  23.555   9.446  1.00 16.05
ATOM   3139  OH2 TIP C  14      18.354  26.505  28.719  1.00 14.14
ATOM   3140  OH2 TIP C  15      33.073  10.884  15.835  1.00 14.30
ATOM   3141  OH2 TIP C  16      15.032  34.698  31.070  1.00 11.96
ATOM   3142  OH2 TIP C  17       7.170  35.908  33.277  1.00 16.70
ATOM   3143  OH2 TIP C  19      16.624  32.704  28.166  1.00 15.10
ATOM   3144  OH2 TIP C  20      35.078  42.552  29.609  1.00 19.72
ATOM   3145  OH2 TIP C  21      40.457  30.360  27.755  1.00 16.31
ATOM   3146  OH2 TIP C  22      52.263  20.430   9.725  1.00 20.11
ATOM   3147  OH2 TIP C  23      20.720  20.412  14.822  1.00 12.68
ATOM   3148  OH2 TIP C  24      33.413  15.317  -5.393  1.00 15.90
ATOM   3149  OH2 TIP C  25      38.275  25.072  23.469  1.00 13.40
ATOM   3150  OH2 TIP C  27      16.591  21.729   7.186  1.00 19.86
ATOM   3151  OH2 TIP C  28      21.798  19.346  19.780  1.00 14.31
ATOM   3152  OH2 TIP C  29      17.533  34.724  25.177  1.00 16.69
ATOM   3153  OH2 TIP C  30      29.162  27.768  25.821  1.00 19.19
ATOM   3154  OH2 TIP C  31      40.631  28.021  16.946  1.00 14.53
ATOM   3155  OH2 TIP C  32      32.428  32.415  17.998  1.00 10.42
ATOM   3156  OH2 TIP C  33      11.884  34.798  21.161  1.00 23.00
ATOM   3157  OH2 TIP C  34      27.837  25.769  -5.173  1.00 33.18
ATOM   3158  OH2 TIP C  35      12.372  31.279  28.339  1.00 16.96
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ATOM   3159  OH2 TIP C  36      39.263  28.648  25.755  1.00  9.84
ATOM   3160  OH2 TIP C  40      38.924  30.840  30.171  1.00 13.35
ATOM   3161  OH2 TIP C  41      18.085  18.989  18.858  1.00 16.60
ATOM   3162  OH2 TIP C  42       7.300  35.692  30.168  1.00 19.22
ATOM   3163  OH2 TIP C  43      14.250  32.017  30.405  1.00 18.32
ATOM   3164  OH2 TIP C  44      37.440  22.761   1.333  1.00 23.96
ATOM   3165  OH2 TIP C  45      29.932  39.949  32.969  1.00 22.64
ATOM   3166  OH2 TIP C  46      29.433  17.902  20.935  1.00 16.15
ATOM   3167  OH2 TIP C  47      53.536  22.468  21.774  1.00 21.62
ATOM   3168  OH2 TIP C  48      40.180  15.699  -0.272  1.00 12.15
ATOM   3169  OH2 TIP C  49      14.955  25.973  25.745  1.00 11.98
ATOM   3170  OH2 TIP C  50      38.595   6.527   3.885  1.00 23.66
ATOM   3171  OH2 TIP C  51      48.551  24.793  17.574  1.00 18.30
ATOM   3172  OH2 TIP C  52      20.747  27.407  17.869  1.00  8.25
ATOM   3173  OH2 TIP C  53      26.489  18.730  30.746  1.00 26.59
ATOM   3174  OH2 TIP C  54      38.723  11.162  19.249  1.00 11.49
ATOM   3175  OH2 TIP C  55      33.881  26.191  31.382  1.00 19.21
ATOM   3176  OH2 TIP C  56      13.322  31.213  40.027  1.00 15.61
ATOM   3177  OH2 TIP C  57      19.497  16.134  41.439  1.00 26.82
ATOM   3178  OH2 TIP C  58      38.469  37.062   5.695  1.00 23.10
ATOM   3179  OH2 TIP C  59      45.575  15.894   3.122  1.00 18.45
ATOM   3180  OH2 TIP C  60      39.615  25.333  -1.743  1.00 20.09
ATOM   3181  OH2 TIP C  61      32.158  37.928  32.431  1.00 12.17
ATOM   3182  OH2 TIP C  62      46.793  19.609  22.823  1.00 19.81
ATOM   3183  OH2 TIP C  63      24.847  37.031  -0.659  1.00 29.98
ATOM   3184  OH2 TIP C  64      45.957  18.715   3.836  1.00 18.88
ATOM   3185  OH2 TIP C  65      36.189  33.100  17.653  1.00 10.63
ATOM   3186  OH2 TIP C  66      31.177  25.020  24.150  1.00 28.40
ATOM   3187  OH2 TIP C  67      46.181  23.210  18.466  1.00 20.41
ATOM   3188  OH2 TIP C  68      21.756  10.923   7.943  1.00 22.80
ATOM   3189  OH2 TIP C  69      12.936  36.695  30.481  1.00 17.63
ATOM   3190  OH2 TIP C  70      33.713  44.843   8.382  1.00 30.49
ATOM   3191  OH2 TIP C  71      21.051  41.550  39.982  1.00 31.15
ATOM   3192  OH2 TIP C  72      26.815  38.732   3.198  1.00 22.61
ATOM   3193  OH2 TIP C  73      41.656  24.820  21.177  1.00 19.69
ATOM   3194  OH2 TIP C  74      25.521  30.139  47.617  1.00 31.08
ATOM   3195  OH2 TIP C  75      20.497  46.537  15.336  1.00 29.67
ATOM   3196  OH2 TIP C  76       7.708  28.422  41.027  1.00 26.00
ATOM   3197  OH2 TIP C  77      25.650  18.585  27.821  1.00 17.30
ATOM   3198  OH2 TIP C  78      35.124  16.582  21.374  1.00 15.44
ATOM   3199  OH2 TIP C  79      16.806  29.258  45.952  1.00 22.64
ATOM   3200  OH2 TIP C  80      29.365   7.305  14.767  1.00 28.00
ATOM   3201  OH2 TIP C  81      36.259   9.577  -0.018  1.00 36.72
ATOM   3202  OH2 TIP C  82       5.598  37.375  35.367  1.00 29.64
ATOM   3203  OH2 TIP C  83      14.256  22.267   9.863  1.00 20.30
ATOM   3204  OH2 TIP C  84      34.533  14.826  41.318  1.00 35.70
ATOM   3205  OH2 TIP C  85      14.253  38.931  17.469  1.00 22.15
ATOM   3206  OH2 TIP C  86      40.762  43.633   8.075  1.00 32.27
ATOM   3207  OH2 TIP C  87      20.139  38.471  47.202  1.00 19.79
ATOM   3208  OH2 TIP C  88      49.003  25.388  14.809  1.00 16.95
ATOM   3209  OH2 TIP C  89      48.376  21.580  21.346  1.00 26.51
ATOM   3210  OH2 TIP C  90      38.281  15.314  27.561  1.00 34.16
ATOM   3211  OH2 TIP C  91       8.631  39.984  34.095  1.00 41.37
ATOM   3212  OH2 TIP C  92      50.906  23.612  20.744  1.00 52.18
ATOM   3213  OH2 TIP C  93      53.785  20.060  24.538  1.00 24.16
ATOM   3214  OH2 TIP C  94      24.823  42.619  11.579  1.00 21.18
ATOM   3215  OH2 TIP C  95      25.075  45.083   6.146  1.00 38.65
ATOM   3216  OH2 TIP C  96      40.830  25.584  18.443  1.00 18.31
ATOM   3217  OH2 TIP C  97      43.416  22.239  18.182  1.00 19.16
ATOM   3218  OH2 TIP C  98      13.417  34.174  40.223  1.00 31.15
ATOM   3219  OH2 TIP C  99      33.278  34.940  35.258  1.00 19.39
ATOM   3220  OH2 TIP C 100      16.214  11.125  16.638  1.00 44.74
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ATOM   3221  OH2 TIP C 101      53.364  20.723  14.579  1.00 34.15
ATOM   3222  OH2 TIP C 102      49.883  22.898   7.975  1.00 17.76
ATOM   3223  OH2 TIP C 103      23.025  15.361  39.364  1.00 32.71
ATOM   3224  OH2 TIP C 104       9.989  41.920  29.368  1.00 18.54
ATOM   3225  OH2 TIP C 105      40.434  26.276  24.857  1.00 17.36
ATOM   3226  OH2 TIP C 106      20.997  29.964   6.095  1.00 20.90
ATOM   3227  OH2 TIP C 107      27.762  47.336  16.035  1.00 24.48
ATOM   3228  OH2 TIP C 108      49.284  22.771   5.126  1.00 18.73
ATOM   3229  OH2 TIP C 109      48.838  23.239  29.592  1.00 33.97
ATOM   3230  OH2 TIP C 110      28.582  23.099  35.349  1.00 20.25
ATOM   3231  OH2 TIP C 111      32.528  35.162  39.110  1.00 29.39
ATOM   3232  OH2 TIP C 112      41.404  21.066  27.696  1.00 29.24
ATOM   3233  OH2 TIP C 113      41.566  30.795  24.916  1.00 29.04
ATOM   3234  OH2 TIP C 114      38.888  34.349   4.634  1.00 19.24
ATOM   3235  OH2 TIP C 115      21.524  13.318   6.181  1.00 21.83
ATOM   3236  OH2 TIP C 116      20.262  44.365  41.166  1.00 51.68
ATOM   3237  OH2 TIP C 117      40.866  37.586   7.262  1.00 26.48
ATOM   3238  OH2 TIP C 118      24.269  19.013  20.381  1.00 20.56
ATOM   3239  OH2 TIP C 119      14.796  40.366  21.026  1.00 26.21
ATOM   3240  OH2 TIP C 120      40.271  21.968  24.452  1.00 22.99
ATOM   3241  OH2 TIP C 121      27.256   8.206   3.568  1.00 32.16
ATOM   3242  OH2 TIP C 122      38.453  23.426  21.155  1.00 20.65
ATOM   3243  OH2 TIP C 123      39.489  30.192  18.787  1.00 19.64
ATOM   3244  OH2 TIP C 124      49.479  24.877   3.120  1.00 15.38
ATOM   3245  OH2 TIP C 125      23.534  17.922  36.838  1.00 21.55
ATOM   3246  OH2 TIP C 126      24.481  13.568  37.531  1.00 33.00
ATOM   3247  OH2 TIP C 127      27.515  37.075  45.132  1.00 32.65
ATOM   3248  OH2 TIP C 128      20.903  11.530  10.774  1.00 25.13
ATOM   3249  OH2 TIP C 129      16.996  37.117   6.834  1.00 26.72
ATOM   3250  OH2 TIP C 130      42.280  39.848   5.806  1.00 39.08
ATOM   3251  OH2 TIP C 131      15.426  37.238  14.643  1.00 27.36
ATOM   3252  OH2 TIP C 132      47.740  29.973  16.321  1.00 27.58
ATOM   3253  OH2 TIP C 133      52.162  19.864  18.278  1.00 19.10
ATOM   3254  OH2 TIP C 134      47.805  11.416   4.529  1.00 30.40
ATOM   3255  OH2 TIP C 135      20.920  22.905  41.964  1.00 23.80
ATOM   3256  OH2 TIP C 136      27.784  19.013  -1.506  1.00 28.71
ATOM   3257  OH2 TIP C 137      25.506  36.437   2.115  1.00 19.53
ATOM   3258  OH2 TIP C 138       6.347  36.058  44.801  1.00 30.54
ATOM   3259  OH2 TIP C 139      18.428  23.862   8.397  1.00 19.65
ATOM   3260  OH2 TIP C 140      56.631  14.945  24.048  1.00 29.26
ATOM   3261  OH2 TIP C 141      36.045  33.381  -3.424  1.00 39.63
ATOM   3262  OH2 TIP C 142      20.242  14.180  11.802  1.00 31.49
ATOM   3263  OH2 TIP C 143       8.614  22.301  31.526  1.00 30.94
ATOM   3264  OH2 TIP C 144       8.697  38.736  31.440  1.00 44.64
ATOM   3265  OH2 TIP C 145      21.002  20.115  40.621  1.00 23.34
ATOM   3266  OH2 TIP C 146      36.343  37.533   7.628  1.00 25.43
ATOM   3267  OH2 TIP C 147      13.944  44.970  51.125  1.00 40.01
ATOM   3268  OH2 TIP C 148      12.509  22.964  23.735  1.00 33.44
ATOM   3269  OH2 TIP C 149      32.555   6.398   6.686  1.00 30.50
ATOM   3270  OH2 TIP C 150      11.123  30.018  41.695  1.00 29.12
ATOM   3271  OH2 TIP C 151      20.406  19.454  17.419  1.00 26.72
ATOM   3272  OH2 TIP C 152      37.729  21.375  25.750  1.00 27.16
ATOM   3273  OH2 TIP C 153      36.922  28.170  33.507  1.00 42.28
ATOM   3274  OH2 TIP C 154      13.904  29.766  32.277  1.00 19.72
ATOM   3275  OH2 TIP C 155      54.556  19.732  11.775  1.00 37.67
ATOM   3276  OH2 TIP C 156      14.999  28.327  48.310  1.00 40.64
ATOM   3277  OH2 TIP C 157      19.001  46.759  12.106  1.00 40.48
ATOM   3278  OH2 TIP C 158      22.361   9.339  13.691  1.00 44.57
ATOM   3279  OH2 TIP C 159      26.097  16.601  36.996  1.00 27.61
ATOM   3280  OH2 TIP C 160      51.862  24.669  14.501  1.00 39.22
ATOM   3281  OH2 TIP C 161      42.713  33.316  38.299  1.00 37.21
ATOM   3282  OH2 TIP C 162      32.074  43.316   6.583  1.00 32.14
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ATOM	3283	OH2	TIP	C	163	44.434	22.056	2.693	1.00	44.76
ATOM	3284	OH2	TIP	C	164	24.074	33.090	45.770	1.00	26.95
ATOM	3285	OH2	TIP	C	165	12.289	35.656	48.500	1.00	33.30
ATOM	3286	OH2	TIP	C	166	19.499	27.253	51.538	1.00	48.93
ATOM	3287	OH2	TIP	C	167	28.896	14.390	20.410	1.00	32.12
ATOM	3288	OH2	TIP	C	168	7.799	34.543	25.107	1.00	34.11
ATOM	3289	OH2	TIP	C	169	41.359	33.697	5.939	1.00	29.72
ATOM	3290	OH2	TIP	C	170	26.378	23.008	46.449	1.00	37.54
ATOM	3291	OH2	TIP	C	171	10.530	41.770	49.010	1.00	34.66
ATOM	3292	OH2	TIP	C	172	41.154	5.586	4.533	1.00	25.18
ATOM	3293	OH2	TIP	C	173	17.462	11.487	4.521	1.00	46.32
ATOM	3294	OH2	TIP	C	174	7.600	39.527	37.113	1.00	36.37
ATOM	3295	OH2	TIP	C	175	3.552	23.235	37.583	1.00	39.37
ATOM	3296	OH2	TIP	C	176	32.818	21.891	40.191	1.00	36.81
ATOM	3297	OH2	TIP	C	177	30.404	26.159	40.588	1.00	38.22
ATOM	3298	OH2	TIP	C	178	16.691	29.183	54.400	1.00	39.76
ATOM	3299	OH2	TIP	C	179	16.247	47.986	22.417	1.00	32.19
ATOM	3300	OH2	TIP	C	180	37.394	44.558	11.594	1.00	39.03
ATOM	3301	OH2	TIP	C	181	53.552	27.209	11.822	1.00	47.97
ATOM	3302	OH2	TIP	C	182	10.503	32.709	12.025	1.00	38.41
ATOM	3303	OH2	TIP	C	183	17.985	14.916	28.259	1.00	36.86
ATOM	3304	OH2	TIP	C	184	25.047	45.446	12.174	1.00	49.92
ATOM	3305	OH2	TIP	C	185	16.402	15.741	36.532	1.00	40.29
ATOM	3306	OH2	TIP	C	186	51.364	22.471	17.335	1.00	28.11
ATOM	3307	OH2	TIP	C	187	25.633	28.369	50.282	1.00	42.57
ATOM	3308	OH2	TIP	C	188	35.183	14.816	0.037	1.00	36.60
ATOM	3309	OH2	TIP	C	189	8.318	26.536	23.386	1.00	44.75
ATOM	3310	OH2	TIP	C	190	47.893	17.794	24.745	1.00	42.51
ATOM	3311	OH2	TIP	C	191	2.728	32.293	36.650	1.00	38.36
ATOM	3312	OH2	TIP	C	192	30.315	9.929	15.860	1.00	39.58
ATOM	3313	OH2	TIP	C	193	29.613	40.378	2.225	1.00	41.26
ATOM	3314	OH2	TIP	C	194	14.241	43.934	16.316	1.00	43.60
ATOM	3315	OH2	TIP	C	195	48.673	31.215	7.801	1.00	32.67
ATOM	3316	OH2	TIP	C	196	10.948	21.963	18.969	1.00	41.87
ATOM	3317	OH2	TIP	C	197	37.378	39.077	3.714	1.00	35.77
ATOM	3318	OH2	TIP	C	198	24.488	11.993	21.654	1.00	38.05
ATOM	3319	OH2	TIP	C	199	47.986	31.378	4.946	1.00	48.02
ATOM	3320	OH2	TIP	C	200	15.373	46.520	15.659	1.00	45.30
ATOM	3321	OH2	TIP	C	201	29.464	40.417	40.154	1.00	40.62
ATOM	3322	OH2	TIP	C	202	56.018	18.652	7.189	1.00	43.28
ATOM	3323	OH2	TIP	C	203	36.508	17.526	41.765	1.00	61.21
ATOM	3324	OH2	TIP	C	204	36.132	36.523	-0.637	1.00	43.56
ATOM	3325	OH2	TIP	C	205	9.832	29.974	46.230	1.00	47.33
ATOM	3326	OH2	TIP	C	206	12.086	37.731	18.949	1.00	44.12
ATOM	3327	OH2	TIP	C	207	4.729	26.744	22.711	1.00	40.03
ATOM	3328	OH2	TIP	C	208	9.555	36.540	23.357	1.00	46.94
ATOM	3329	OH2	TIP	C	209	23.046	47.732	4.343	1.00	48.13
ATOM	3330	OH2	TIP	C	210	39.932	44.592	5.460	1.00	64.51
ATOM	3331	OH2	TIP	C	211	17.996	41.071	6.267	1.00	48.35
ATOM	3332	OH2	TIP	C	212	17.866	46.493	17.139	1.00	39.09
ATOM	3333	OH2	TIP	C	213	55.520	11.908	17.658	1.00	43.06
ATOM	3334	OH2	TIP	C	214	3.059	35.093	42.826	1.00	38.97
ATOM	3335	OH2	TIP	C	215	31.593	14.910	43.677	1.00	44.01
ATOM	3336	OH2	TIP	C	216	33.045	23.673	44.607	1.00	45.50
ATOM	3337	OH2	TIP	C	217	42.870	35.555	7.510	1.00	29.79
ATOM	3338	OH2	TIP	C	218	4.112	25.648	42.564	1.00	56.65
ATOM	3339	OH2	TIP	C	219	48.260	8.547	20.446	1.00	47.85
ATOM	3340	OH2	TIP	C	220	-0.925	31.171	41.173	1.00	36.99
ATOM	3341	OH2	TIP	C	221	41.791	22.878	0.132	1.00	56.14
ATOM	3342	OH2	TIP	C	222	7.088	25.685	41.540	1.00	47.43
ATOM	3343	OH2	TIP	C	223	24.815	4.785	13.582	1.00	47.96
ATOM	3344	OH2	TIP	C	224	40.690	4.520	15.174	1.00	48.76

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ATOM   3345  OH2 TIP C 225      10.029  32.425  18.562  1.00 36.30
ATOM   3346  OH2 TIP C 226      22.346  37.737  48.941  1.00 34.15
ATOM   3347  OH2 TIP C 227      16.274  17.012  19.693  1.00 27.63
ATOM   3348  OH2 TIP C 228      35.332  13.692  20.375  1.00 37.59
ATOM   3349  OH2 TIP C 229      41.228  36.673  22.908  1.00 51.58
ATOM   3350  OH2 TIP C 230      17.416  42.030  50.226  1.00 47.63
ATOM   3351  OH2 TIP C 231      18.428  39.213  52.835  1.00 40.43
ATOM   3352  OH2 TIP C 232      42.243  43.386  25.548  1.00 48.60
ATOM   3353  OH2 TIP C 233      14.081  18.701   0.364  1.00 32.87
ATOM   3354  OH2 TIP C 234      41.421  41.332  28.531  1.00 54.67
ATOM   3355  OH2 TIP C 235      42.772  36.396  11.892  1.00 41.24
ATOM   3356  OH2 TIP C 236      13.068  13.733  28.653  1.00 42.66
ATOM   3357  OH2 TIP C 237      10.850  26.738   7.811  1.00 40.46
ATOM   3358  OH2 TIP C 238      16.253  20.926  45.776  1.00 44.60
ATOM   3359  OH2 TIP C 239      32.681  31.139  43.220  1.00 42.20
ATOM   3360  OH2 TIP C 240      56.267  22.254   9.280  1.00 52.44
ATOM   3361  OH2 TIP C 241      12.553  25.304   9.942  1.00 38.77
ATOM   3362  OH2 TIP C 242      50.727   9.516  16.775  1.00 33.38
ATOM   3363  OH2 TIP C 243      31.871  41.347   0.512  1.00 47.78
ATOM   3364  OH2 TIP C 244      10.008  45.092  37.807  1.00 39.52
ATOM   3365  OH2 TIP C 245      14.551  39.030   6.708  1.00 44.26
ATOM   3366  OH2 TIP C 246      26.955  18.903  -5.135  1.00 42.54
ATOM   3367  OH2 TIP C 247      39.916  22.478  18.854  1.00 33.22
ATOM   3368  OH2 TIP C 248      40.431  40.824  22.426  1.00 35.58
ATOM   3369  OH2 TIP C 249      52.081  23.408  10.759  1.00 42.53
ATOM   3370  OH2 TIP C 250      12.078  16.710  24.149  1.00 32.37
ATOM   3371  OH2 TIP C 251      54.111  15.908   8.256  1.00 44.58
ATOM   3372  OH2 TIP C 252      33.950  12.827  -1.753  1.00 27.02
ATOM   3373  OH2 TIP C 253      -0.775  26.703  40.353  1.00 43.64
ATOM   3374  OH2 TIP C 254       1.937  33.711  40.561  1.00 42.67
ATOM   3375  OH2 TIP C 255       8.008  24.066  18.824  1.00 51.45
ATOM   3376  OH2 TIP C 256      11.765  27.465   3.635  1.00 47.34
ATOM   3377  OH2 TIP C 257      27.863  43.878   9.233  1.00 32.44
ATOM   3378  OH2 TIP C 258      18.655  30.114   4.303  1.00 33.13
ATOM   3379  OH2 TIP C 259      21.592  19.085  -3.960  1.00 39.86
ATOM   3380  OH2 TIP C 260      41.876  24.067  25.906  1.00 26.34
ATOM   3381  OH2 TIP C 261      46.651  10.240   2.171  1.00 44.38
ATOM   3382  OH2 TIP C 262      32.536  15.827  32.477  1.00 43.28
ATOM   3383  OH2 TIP C 263      12.479  39.205  50.359  1.00 47.33
ATOM   3384  OH2 TIP C 264       0.850  27.980  38.316  1.00 43.45
ATOM   3385  OH2 TIP C 265      49.605   7.356  18.061  1.00 66.01
ATOM   3386  OH2 TIP C 266      30.177  40.365  -3.235  1.00 44.45
ATOM   3387  OH2 TIP C 267      39.818  12.364   0.512  1.00 48.84
ATOM   3388  OH2 TIP C 268      38.149  44.716  27.884  1.00 51.18
ATOM   3389  OH2 TIP C 269      37.156  37.062  30.528  1.00 35.17
ATOM   3390  OH2 TIP C 270      51.808   7.097  12.435  1.00 51.69
ATOM   3391  OH2 TIP C 271      54.351  12.626  12.471  1.00 47.45
ATOM   3392  OH2 TIP C 272      50.835  31.155  13.092  1.00 55.05
ATOM   3393  OH2 TIP C 273      12.159  35.313  52.133  1.00 52.38
ATOM   3394  OH2 TIP C 274      21.002  44.489  13.037  1.00 39.70
ATOM   3395  OH2 TIP C 275      37.936  23.627  34.221  1.00 48.56
ATOM   3396  OH2 TIP C 276      45.844  30.935  31.365  1.00 43.24
ATOM   3397  OH2 TIP C 277      38.831  48.015  15.554  1.00 49.83
ATOM   3398  OH2 TIP C 278       5.630  28.150  44.576  1.00 48.10
ATOM   3399  OH2 TIP C 279       8.600  24.000  45.727  1.00 49.27
ATOM   3400  OH2 TIP C 280      54.276  20.854   7.807  1.00 36.02
ATOM   3401  OH2 TIP C 281       3.544  34.696  46.365  1.00 43.63
ATOM   3402  OH2 TIP C 282      24.214  46.264  46.163  1.00 48.04
ATOM   3403  OH2 TIP C 283       7.099  32.072  19.549  1.00 54.97
ATOM   3404  OH2 TIP C 284      36.469  22.374  41.355  1.00 52.17
ATOM   3405  OH2 TIP C 285      34.660  13.757  23.756  1.00 45.46
ATOM   3406  OH2 TIP C 286      28.516  42.981   5.402  1.00 53.58
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ATOM   3407  OH2 TIP C 287      35.579   4.929  12.012  1.00 52.07
ATOM   3408  OH2 TIP C 288      22.974  49.682  24.299  1.00 53.67
ATOM   3409  OH2 TIP C 289       3.725  31.464  46.354  1.00 46.43
ATOM   3410  OH2 TIP C 290      27.340  39.594  -2.191  1.00 56.89
ATOM   3411  OH2 TIP C 291      33.413  34.856  32.335  1.00 31.78
ATOM   3412  OH2 TIP C 292      43.340   7.715   8.063  1.00 43.53
ATOM   3413  OH2 TIP C 293      28.243  21.392  -4.937  1.00 38.33
ATOM   3414  OH2 TIP C 294      49.389  26.590  35.796  1.00 45.66
ATOM   3415  OH2 TIP C 295      28.948  15.824  33.796  1.00 52.48
ATOM   3416  OH2 TIP C 296      27.347  13.383  37.207  1.00 48.27
ATOM   3417  OH2 TIP C 297      38.485  26.090  36.901  1.00 48.92
ATOM   3418  OH2 TIP C 298      12.120  20.265  11.506  1.00 50.10
ATOM   3419  OH2 TIP C 299      36.480  36.306  38.613  1.00 50.38
ATOM   3420  OH2 TIP C 300      31.471  16.463  35.507  1.00 38.37
ATOM   3421  OH2 TIP C 301      42.889   5.274   2.358  1.00 33.49
ATOM   3422  OH2 TIP C 302      23.548  44.173  32.246  1.00 39.09
ATOM   3423  OH2 TIP C 303      13.465  43.978  13.054  1.00 52.67
ATOM   3424  OH2 TIP C 304      25.133  43.053   4.111  1.00 52.03
ATOM   3425  OH2 TIP C 305      33.587  24.652  39.392  1.00 49.48
ATOM   3426  OH2 TIP C 306      39.063  28.353   1.979  1.00 47.89
ATOM   3427  OH2 TIP C 307      49.357  35.834  12.150  1.00 49.22
ATOM   3428  OH2 TIP C 308      27.159  46.386  33.347  1.00 49.50
ATOM   3429  OH2 TIP C 309       9.510  21.769  39.704  1.00 47.95
ATOM   3430  OH2 TIP C 310      34.885  32.959  39.205  1.00 51.26
ATOM   3431  OH2 TIP C 311      30.980   6.002   9.747  1.00 56.02
ATOM   3432  OH2 TIP C 312      43.802  34.511  14.853  1.00 41.89
ATOM   3433  OH2 TIP C 313      36.834   4.382   5.254  1.00 39.04
ATOM   3434  OH2 TIP C 314      12.453  30.429  47.461  1.00 47.60
ATOM   3435  OH2 TIP C 315      39.685  40.144  30.944  1.00 54.68
ATOM   3436  OH2 TIP C 316      45.982  20.840  31.078  1.00 47.99
ATOM   3437  OH2 TIP C 317      32.815  36.023  42.050  1.00 45.07
ATOM   3438  OH2 TIP C 318      17.877  37.802  -3.699  1.00 56.30
ATOM   3439  OH2 TIP C 319      53.681   9.633  16.525  1.00 55.34
ATOM   3440  OH2 TIP C 320      21.577  43.070  52.229  1.00 49.54
ATOM   3441  OH2 TIP C 321       6.139  45.122  36.565  1.00 44.40
ATOM   3442  OH2 TIP C 322      34.695  13.561  26.782  1.00 45.99
ATOM   3443  OH2 TIP C 323      17.990  33.946  -9.976  1.00 56.88
ATOM   3444  OH2 TIP C 324      25.587  50.416  28.268  1.00 52.75
ATOM   3445  OH2 TIP C 325      27.744  42.608  42.266  1.00 44.66
ATOM   3446  OH2 TIP C 326      48.357  32.815  33.851  1.00 57.98
ATOM   3447  OH2 TIP C 327      61.047  18.004  17.692  1.00 51.30
ATOM   3448  OH2 TIP C 328      17.327  11.069  11.972  1.00 48.28
ATOM   3449  OH2 TIP C 329      59.624  17.562  20.598  1.00 44.37
ATOM   3450  OH2 TIP C 330      40.644  39.227  19.932  1.00 37.57
ATOM   3451  OH2 TIP C 331      12.920  31.214  52.942  1.00 51.07
ATOM   3452  OH2 TIP C 332      37.639   0.847  19.561  1.00 49.44
ATOM   3453  OH2 TIP C 333      34.243  38.790  -3.251  1.00 54.21
ATOM   3454  OH2 TIP C 334      24.216  47.874   6.983  1.00 50.90
ATOM   3455  OH2 TIP C 335      15.324  34.797   6.670  1.00 45.25
ATOM   3456  OH2 TIP C 336      18.474  15.525  21.402  1.00 34.12
ATOM   3457  OH2 TIP C 337      40.048   8.873  26.818  1.00 49.89
ATOM   3458  OH2 TIP C 338      32.472  13.331  20.523  1.00 29.86
ATOM   3459  OH2 TIP C 339      57.778  14.167  30.422  1.00 49.76
ATOM   3460  OH2 TIP C 340      46.651  35.476  13.375  1.00 56.48
ATOM   3461  OH2 TIP C 341      15.427  13.237   3.552  1.00 57.25
ATOM   3462  OH2 TIP C 342      40.349  38.972   3.722  1.00 65.27
ATOM   3463  OH2 TIP C 343       8.685  28.945  15.205  1.00 59.60
ATOM   3464  OH2 TIP C 344      11.958  41.585  22.587  1.00 37.18
ATOM   3465  OH2 TIP C 345       9.054  20.498  28.914  1.00 42.95
ATOM   3466  OH2 TIP C 346      20.086  20.088  46.913  1.00 42.03
ATOM   3467  OH2 TIP C 347      40.370  35.093   2.009  1.00 49.35
ATOM   3468  OH2 TIP C 348      41.948   4.327  12.147  1.00 50.59
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ATOM   3469  OH2 TIP C 349      23.518  45.701  40.287  1.00 39.79
ATOM   3470  OH2 TIP C 350      19.169  37.474   4.786  1.00 44.67
ATOM   3471  OH2 TIP C 351      32.946  39.184  41.062  1.00 57.56
ATOM   3472  OH2 TIP C 352      37.578  47.817  18.421  1.00 51.80
ATOM   3473  OH2 TIP C 353      15.391  43.820   7.645  1.00 58.15
ATOM   3474  OH2 TIP C 354      38.205  17.257  33.401  1.00 55.84
ATOM   3475  OH2 TIP C 355      43.224   1.565  14.606  1.00 41.12
ATOM   3476  OH2 TIP C 356      18.704  51.623  28.487  1.00 61.11
ATOM   3477  OH2 TIP C 357      46.033   5.813   0.173  1.00 43.43
ATOM   3478  OH2 TIP C 358      51.950  27.722  14.408  1.00 45.00
ATOM   3479  OH2 TIP C 359      46.825   2.427  15.714  1.00 52.68
ATOM   3480  OH2 TIP C 360      17.624  50.111  20.315  1.00 39.65
ATOM   3481  O   HOH C 361      27.534  15.877  26.687  1.00 20.00
ATOM   3482  O   HOH C 362      28.946  16.344  30.514  1.00 20.00
END
```

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/29387

A. CLASSIFICATION OF SUBJECT MATTER
IPC(7) : G01N 33/483
US CL : 702/19
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 702/17, 435, 424.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ROSSJOHN et al. Crystal structure of the N-terminal, growth factor-like domain of Alzheimer amyloid precursor protein. Nature Structural Biology. April 1999, Vol 6. No. 4, pages 327-331, see entire document and especially page 330 in Methods.	1-2
Y	ZHANG Z. et al. Sequence-specific recognition of the interanalization motif of the Alzheimer's amyloid precursor protein by the X11 PTB domain. The EMBO Journal. 1997, Vol 16. No. 20, pages 6141-6150, see entire document and especially page 6147.	1-2
Y,P	MARCINKEVICIENE J. at al. Mechanism of Inhibition of beta-Site Amyloid Precursor Protein-cleaving Enzyme (BACE) by a Statine-based Peptide. The Journal of Biological Chemistry. 29 June 2001, Vol 276, No. 26, pages 23790-23794, see entire document.	1
Y	HYNES et al. X-ray Crystal Structure of the Protease Inhibitor Domain of Alzheimer's Amyloid beta-Protein Precursor. Biochemistry.1990, Vol 29, pages 10018-10022, especially page 10019.	1-2

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18 December 2001 (18.12.2001)	13 FEB 2002
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Jaya Bridges NIKOLAI M. GALITSKY PhD. Telephone No. (703)-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/29387

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BAILEY et al. X-ray-crystallographic studies of complexes of pepstatin A and a statine-containing human renin inhibitor with endothiapepsin. Biochem. J.1993, Vol 289, pages 363-371, especialy pages 365-366.	1-2
Y	SCHEIDIG et al. Crystal structures of bovin chymotrypsin and trypsin complexed to the inhibitor domain of Alzheimer's amyloid beta-protein precursor (APPI) and basic pancreatic trypsin inhibitor (BPTI): Engineering of inhibitors wth altered specificities. The Protein Society. September 1997, Vol 6, pages 1806-1824, see entire document and especially page 1820.	1-2
A	KOHNO et al. Thre-Dimentional Structure of the Amyloid beta Peptide (25-35) in Membrane-Mimicking Environment. Biochemistry. 1996, Vol 35, pages 16094-16104, see entire document.	1-2
A	VASSAR et al. Beta-Secretase Cleavage of Azheimer's Amyloid Precursor Protein by the Transmembrane Aspartic Protease BACE. Science. 22 October 1999, Vol 286, pages 735-741, see entire document.	1-2
A	HONG, L. et al. Structure of the Protease Domain of Memapsin 2(beta-Secretase) Complexed with Inhibitor. Science. 24 May 2000, Vol 290, No. 5489, pages 150-159, see entire document	1-2
A	SAUDER, M. et al. Modeling of substrate specifity of the Alzheimer's desease amyloid precursor protein beta-secretase. J. Mol. Biol. 2000, Vol 300, No. 2, pages 241-248, see entire document.	1-2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/29387

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 1 and 2

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/29387

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Invention I and II are directed to different chemical and physical types regarding the critical limitations therein. For Group I, the critical feature is a crystallization of complex whereas for Group II the critical feature is the obtaining or synthesizing the agent. This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Group I, claims 1-2, drawn to crystallized complex.

Group II, claims 24 and 27 drawn to method further comprising one of the steps: obtaining and synthesizing the agen. Claims 3-23, 25,26,28-30 are directed solely to information and are therefore excluded from search.

The International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for reasons indicated below:

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Invention I and II are directed to different chemical and physical types regarding the critical limitations therein. For Group I, the critical feature is a crystallization of complex whereas for Group II the critical feature is the obtaining or synthesizing the agent.

Continuation of B. FIELDS SEARCHED Item 3:

WEST, STN, Non-patent-literature covering search terms: Cleaving Enzyme(BACE), crystallization, beta-Amyloid Precursor protein, 3-d structure of APP, Statine-based peptides.